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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:58:19 ; Search time 0.880829 Seconds
(without alignments)
287.324 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94

Sequence: 1 ENPVVHFKNIVTPRT 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:
- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
 - 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	94	100.0	24	7 US-11-045-024-14523	Sequence 14523, A
2	94	100.0	197	7 US-11-090-878-54	Sequence 54, Appl
3	94	100.0	304	7 US-11-033-039-824	Sequence 824, Appl
4	83.5	88.8	30	7 US-11-106-932-11	Sequence 11, Appl
5	82	87.2	15	7 US-11-150-755-1	Sequence 1, Appl
6	79	84.0	15	7 US-11-150-755-69	Sequence 69, Appl
7	76	80.9	16	7 US-11-045-024-14247	Sequence 14247, A
8	66	70.2	12	7 US-11-033-039-822	Sequence 822, A
9	60	63.8	12	6 US-10-893-584-126	Sequence 126, Appl
10	48	51.1	9	7 US-11-033-039-832	Sequence 832, Appl
11	46	48.9	15	7 US-11-106-932-69	Sequence 69, Appl
12	41	43.6	574	7 US-11-072-512-3209	Sequence 3209, Appl
13	39	41.5	337	7 US-11-174-816-43	Sequence 43, Appl
14	39	41.5	337	7 US-11-174-816-43	Sequence 11, Appl
15	39	41.5	1704	7 US-11-075-046-40	Sequence 40, Appl
16	38	40.4	123	7 US-11-195-459-10	Sequence 10, Appl
17	38	40.4	252	7 US-11-012-762-14	Sequence 14, Appl
18	38	40.4	258	6 US-10-467-657-3202	Sequence 3202, Appl
19	38	40.4	318	7 US-11-098-686-10517	Sequence 10517, A
20	38	40.4	376	7 US-11-012-762-10	Sequence 10, Appl
21	38	40.4	376	7 US-11-012-762-16	Sequence 16, Appl
22	38	40.4	376	7 US-11-012-762-18	Sequence 18, Appl
23	38	40.4	376	7 US-11-012-762-20	Sequence 20, Appl
24	38	40.4	376	7 US-11-012-762-24	Sequence 24, Appl
25	38	40.4	376	7 US-11-012-762-40	Sequence 40, Appl

26	37.5	39.9	15	7 US-11-106-932-70	Sequence 70, Appl
27	37.5	39.9	103	6 US-10-467-657-9210	Sequence 9210, Appl
28	37	39.4	121	7 US-11-072-512-3879	Sequence 3879, Appl
29	37	39.4	202	6 US-10-714-887-32	Sequence 32, Appl
30	37	39.4	273	6 US-10-453-372-1062	Sequence 1062, Appl
31	37	39.4	276	6 US-10-453-372-1060	Sequence 1060, Appl
32	37	39.4	300	6 US-10-453-372-1056	Sequence 1056, Appl
33	37	39.4	310	7 US-11-025-834A-13	Sequence 13, Appl
34	37	39.4	329	6 US-10-453-372-1054	Sequence 1054, Appl
35	37	39.4	1798	6 US-10-995-561-1033	Sequence 1033, Appl
36	37	39.4	1798	6 US-10-995-561-1034	Sequence 1034, Appl
37	36	38.3	293	7 US-11-098-686-10871	Sequence 10871, A
38	36	38.3	329	6 US-10-453-372-1058	Sequence 1058, Appl
39	36	38.3	553	7 US-11-040-218-21	Sequence 21, Appl
40	36	38.3	554	7 US-11-098-686-10420	Sequence 10420, A
41	36	38.3	696	7 US-11-080-991-46	Sequence 46, Appl
42	36	38.3	697	7 US-11-100-640-6	Sequence 6, Appl
43	36	38.3	697	7 US-11-100-640-20	Sequence 20, Appl
44	36	38.3	779	7 US-11-186-284-151	Sequence 151, Appl
45	36	38.3	815	7 US-11-072-512-2496	Sequence 2496, Appl

ALIGNMENTS

RESULT 1

US-11-045-024-14523
; Sequence 14523, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14523
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard Peptide 507.02
US-11-045-024-14523

Query Match 100.0%; Score 94; DB 7; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | |
Db 6 ENPVVHFFKNIIVTRTP 22

RESULT 2

US-11-090-878-54

; Sequence 54, Application US/11090878

; Publication No. US2005024911A1

; GENERAL INFORMATION:

; APPLICANT: Saus, Juan

; TITLE OF INVENTION: Methods and Reagents for Identifying Compounds for

; TREATING AUTOIMMUNE DISORDERS

; FILE REFERENCE: 98-723-C3

; CURRENT APPLICATION NUMBER: US/11/090,878

; CURRENT FILING DATE: 2005-03-25

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 54

; LENGTH: 197

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HMBP-21

US-11-090-878-54

Query Match

Best Local Similarity 100.0%; Score 94; DB 7; Length 197;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | |
Db 110 ENPVVHFFKNIIVTRTP 126

RESULT 3

US-11-033-039-824

; Sequence 824, Application US/11033039

; Publication No. US20060002947A1

; GENERAL INFORMATION:

; APPLICANT: HUMPHREYS, ROBERT

; APPLICANT: XU, MINZHEN

; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

; FILE REFERENCE: REH-2017US01

; CURRENT APPLICATION NUMBER: US/11/033,039

; CURRENT FILING DATE: 2005-01-11

; PRIOR APPLICATION NUMBER: 10/245,871

; PRIOR FILING DATE: 2002-09-17

; PRIOR APPLICATION NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: 09/396,813

; PRIOR FILING DATE: 1999-09-14

; NUMBER OF SEQ ID NOS: 1452

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 824

; LENGTH: 304

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-033-039-824

Query Match

Best Local Similarity 100.0%; Score 94; DB 7; Length 304;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | |
Db 217 ENPVVHFFKNIIVTRTP 233

RESULT 4

US-11-106-932-11

; Sequence 11, Application US/11106932

; Publication No. US20050260697A1

; GENERAL INFORMATION:

; APPLICANT: WANG, KA-WANG KEVIN

; APPLICANT: HAYES, RONALD

; APPLICANT: LIU, MING CHEN

; APPLICANT: OLI, MONIKA

; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN

; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING

; FILE REFERENCE: 5853-549-1

; CURRENT APPLICATION NUMBER: US/11/106,932

; CURRENT FILING DATE: 2005-04-15

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Rattus rattus

US-11-106-932-11

Query Match

Best Local Similarity 88.8%; Score 83.5; DB 7; Length 30;

Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | |
Db 8 ENPVVHFFKNIIVTRTP 25

RESULT 5

US-11-150-755-1

; Sequence 1, Application US/11150755

; Publication No. US20060020109A1

; GENERAL INFORMATION:

; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS

; FILE REFERENCE: 24655-017

; CURRENT APPLICATION NUMBER: US/11/150,755

; CURRENT FILING DATE: 2005-06-10

; PRIOR APPLICATION NUMBER: US/10/056,583

; PRIOR FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: 60/263,569

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: DOMAIN

; LOCATION: 85 - 99

; OTHER INFORMATION: Immunodominant peptide of MBP, recognized by

; OTHER INFORMATION: HLA-DR2 haplotype

US-11-150-755-1

Query Match

Best Local Similarity 87.2%; Score 82; DB 7; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 15
| | | | | | | | | | | | | | | | | |
Db 1 ENPVVHFFKNIIVTRTP 15

RESULT 6

US-11-150-755-69

; Sequence 69, Application US/11150755

; Publication No. US20060020109A1

; GENERAL INFORMATION:

; APPLICANT: Strominger, Jack L.

; APPLICANT: Fridkis-Hareli, Masha

```

; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/11/150,755
; CURRENT FILING DATE: 2005-06-10
; PRIOR APPLICATION NUMBER: US/10/056,583
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-11-150-755-69

Query Match      84.9%; Score 79; DB 7; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.7e-07;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIIVTPR 15
      |||||:|||||
DB      1 ENPVVHFFKNIIVTPR 15

RESULT 7
US-11-045-024-14247
; Sequence 14247, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14247
; LENGTH: 16
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14247

Query Match      80.9%; Score 76; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e-07;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VVHFFKNIIVTRTP 17
      |||||:|||||
DB      1 VVHFFKNIIVTRTP 14

RESULT 8
US-11-033-039-822
; Sequence 822, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 822
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-822

Query Match      70.2%; Score 66; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PNVHFFKNIIVTP 14
      |||||:|||||
DB      1 PNVHFFKNIIVTP 12

RESULT 9
US-10-893-584-126
; Sequence 126, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Admir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 126
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutant prepropricin linker region for calpain, pAP-296
US-10-893-584-126

Query Match      63.8%; Score 60; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00027;

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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FFKNIVTPRTP 17
Db 1 FFKNIVTPRTP 11

RESULT 10
US-11-033-039-832
; Sequence 832, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 832
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-832

Query Match 51.1%; Score 48; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VHFKNIVT 13
Db 1 VHFKNIVT 9

RESULT 11
US-11-106-932-69
; Sequence 69, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Rattus rattus
US-11-106-932-69

Query Match 48.9%; Score 46; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFF 8
Db 8 ENPVVHFF 15

RESULT 12
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US-11-072-512-3209
; Sequence 3209, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3209
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3209

Query Match 43.6%; Score 41; DB 7; Length 574;
Best Local Similarity 47.1%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
Db 533 ESPRIHPRTPKTPRTP 549

RESULT 13
US-11-174-816-43
; Sequence 43, Application US/11174816
; Publication No. US20060009441A1
; GENERAL INFORMATION:
; APPLICANT: EBELING, MARTIN
; APPLICANT: HOENER, MARIUS
; APPLICANT: LINDEMANN, LOTHAR
; TITLE OF INVENTION: HUMAN TRACE AMINE ASSOCIATED RECEPTORS
; FILE REFERENCE: 22645
; CURRENT APPLICATION NUMBER: US/11/174,816
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: EP 04103261.6
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 43
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-174-816-43

Query Match 41.5%; Score 39; DB 7; Length 337;
Best Local Similarity 26.7%; Pred. No. 33;
Matches 8; Conservative 5; Mismatches 3; Indels 14; Gaps 1;
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QY 2 NPVHFF-----KNIVTPRTP 17
 ||::: | : ||||
 Db 301 NPIIVFSYRWFKALKLLSREIFSPRT 330

RESULT 14

US-11-174-819-11
 ; Sequence 11, Application US/11174819
 ; Publication No. US20060008880A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EBELING, MARTIN
 ; APPLICANT: HOENER, MARIUS
 ; APPLICANT: LINDEMANN, LOTHAR
 ; TITLE OF INVENTION: MOUSE TRACE AMINE ASSOCIATED RECEPTORS AND
 ; FILE REFERENCE: 22646
 ; CURRENT APPLICATION NUMBER: US/11/174,819
 ; CURRENT FILING DATE: 2005-07-05
 ; PRIOR APPLICATION NUMBER: EP 04103262.4
 ; PRIOR FILING DATE: 2004-07-08
 ; NUMBER OF SEQ ID NOS: 136
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 11
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; FEATURE:
 ; OTHER INFORMATION: mTAARS
 US-11-174-819-11

Query Match 41.5%; Score 39; DB 7; Length 337;
 Best Local Similarity 26.7%; Pred. No. 33;
 Matches 8; Conservative 5; Mismatches 3; Indels 14; Gaps 1;

QY 2 NPVHFF-----KNIVTPRTP 17
 ||::: | : ||||
 Db 301 NPIIVFSYRWFKALKLLSREIFSPRT 330

RESULT 15

US-11-075-046-40
 ; Sequence 40, Application US/11075046
 ; Publication No. US20050268353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
 ; APPLICANT: T. N. HANZLIK
 ; TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
 ; TITLE OF INVENTION: PROTECTING PLANTS
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DORSEY & WHITNEY LLP
 ; STREET: FOUR EMBARCADERO CENTER, SUITE 3400
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES OF AMERICA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/11/075,046
 ; FILING DATE: 07-MAR-2005
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/677,653
 ; FILING DATE: 03-Oct-2000
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: RICHARD F. TRECARTIN
 ; REGISTRATION NUMBER: 31,901
 ; REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC

; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1704 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-11-075-046-40

Query Match 41.5%; Score 39; DB 7; Length 1704;
 Best Local Similarity 40.0%; Pred. No. 2e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PVVHFFKNIVTPRTP 17
 | : | : ||||
 Db 1431 PAANSFSELLTPETP 1445

Search completed: February 22, 2006, 22:03:45
 Job time : 1.88083 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:57:24 ; Search time 8.69085 Seconds
(without alignments)
817.308 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFFKNIVTPRT 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2.6/prodata1/pubpaa/US07_PUBCOMB.pap:*
- 2: /cgn2.6/prodata1/pubpaa/US08_PUBCOMB.pap:*
- 3: /cgn2.6/prodata1/pubpaa/US09_PUBCOMB.pap:*
- 4: /cgn2.6/prodata1/pubpaa/US10A_PUBCOMB.pap:*
- 5: /cgn2.6/prodata1/pubpaa/US10B_PUBCOMB.pap:*
- 6: /cgn2.6/prodata1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	4	US-10-104-973-3
2	94	100.0	17	4	US-10-000-439-13
3	94	100.0	17	4	US-10-362-264-1
4	94	100.0	17	4	US-10-233-892A-2
5	94	100.0	17	5	US-10-482-044-5
6	94	100.0	17	5	US-10-770-712-6
7	94	100.0	19	3	US-09-740-003-2
8	94	100.0	19	3	US-09-768-872-1
9	94	100.0	19	3	US-09-766-378A-32
10	94	100.0	19	4	US-10-239-313A-143
11	94	100.0	19	4	US-10-743-398-2
12	94	100.0	20	3	US-09-766-378A-28
13	94	100.0	20	3	US-09-836-433-30
14	94	100.0	20	3	US-09-859-012-35
15	94	100.0	20	3	US-09-859-012-49
16	94	100.0	21	4	US-10-081-281-33
17	94	100.0	22	5	US-10-492-794-26
18	94	100.0	23	3	US-09-909-460-1
19	94	100.0	23	3	US-09-872-836-1
20	94	100.0	23	3	US-09-906-206A-8
21	94	100.0	23	5	US-10-758-970-1
22	94	100.0	24	4	US-10-149-138-4219
23	94	100.0	24	4	US-10-149-135-2206
24	94	100.0	24	4	US-10-149-138-4219
25	94	100.0	24	4	US-10-149-137A-326
26	94	100.0	24	5	US-10-654-601-2501
27	94	100.0	24	6	US-11-051-411-1220

28	94	100.0	46	3	US-09-813-383-1	Sequence 1, Appli
29	94	100.0	46	3	US-09-813-463A-1	Sequence 1, Appli
30	94	100.0	46	3	US-09-813-463A-1	Sequence 1, Appli
31	94	100.0	123	5	US-10-492-794-115	Sequence 115, App
32	94	100.0	157	4	US-10-425-115-339675	Sequence 339675,
33	94	100.0	169	4	US-10-475-104-32	Sequence 32, Appl
34	94	100.0	169	5	US-10-126-834B-1	Sequence 1, Appli
35	94	100.0	170	4	US-10-015-540-2	Sequence 2, Appli
36	94	100.0	170	4	US-10-199-995-3	Sequence 3, Appli
37	94	100.0	170	5	US-10-773-446-80	Sequence 80, Appl
38	94	100.0	171	2	US-08-484-409-2	Sequence 2, Appli
39	94	100.0	171	3	US-09-989-476-2	Sequence 2, Appli
40	94	100.0	171	3	US-09-947-770-4	Sequence 4, Appli
41	94	100.0	171	3	US-09-893-348-12	Sequence 12, Appl
42	94	100.0	171	3	US-09-218-277-12	Sequence 12, Appl
43	94	100.0	171	4	US-10-104-973-2	Sequence 2, Appli
44	94	100.0	171	4	US-10-000-439-12	Sequence 12, Appl
45	94	100.0	171	4	US-10-270-707-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-104-973-3
; Sequence 3, Application US/10104973
; Publication No. US20020176866A1
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C4
; CURRENT APPLICATION NUMBER: US/10/104,973
; CURRENT FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-10-104-973-3

Query Match 100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
Db 1 ENPVVHFFKNIVTPRT 17

RESULT 2
US-10-000-439-13
; Sequence 13, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-13

Query Match      100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 3
US-10-362-264-1
; Sequence 1, Application US/10362264
; Publication No. US20030191063A1
; GENERAL INFORMATION:
; APPLICANT: Wraith, David
; APPLICANT: Anderton, Stephen
; APPLICANT: Mazza, Graziella
; APPLICANT: Ponsford, Mary
; APPLICANT: Streeter, Heather
; APPLICANT: The University of Bristol
; TITLE OF INVENTION: PEPTIDE SELECTION METHOD
; FILE REFERENCE: 1433.004US1
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03702
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 0020618.5
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 0114547.3
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-264-1

Query Match      100.0%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 4
US-10-233-892A-2
; Sequence 2, Application US/10233892A
; Publication No. US20040043431A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: DIAGNOSIS OF MULTIPLE SCLEROSIS AND
; FILE REFERENCE: OTHER DEMYELINATING DISEASES
; FILE REFERENCE: INSMS.001A
; CURRENT APPLICATION NUMBER: US/10/233.892A
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human Myelin Binding Protein Sequence 83-89
US-10-233-892A-2

Query Match      100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17

US-10-482-044-5
; Sequence 5, Application US/10482044
; Publication No. US20040235713A1
; GENERAL INFORMATION:
; APPLICANT: Anna Maria PAPINI et al
; TITLE OF INVENTION: Glycopeptides, their preparation and use in the diagnosis or
; FILE REFERENCE: 2784 PTWO
; CURRENT APPLICATION NUMBER: US/10/482,044
; CURRENT FILING DATE: 2003-12-22
; PRIOR FILING DATE: PCT/EP 02/06767
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: FI2001A000114
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: glycopeptide
; NAME/KEY: CARBOHYD
; LOCATION: (2)..(2)
; OTHER INFORMATION: the carbohydrate is beta-D-glucopyranosyl
US-10-482-044-5

Query Match      100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
Db      1 ENPVVHFFKNIVTPRTP 17

RESULT 6
US-10-770-712-6
; Sequence 6, Application US/10770712
; Publication No. US2005017033A1
; GENERAL INFORMATION:
; APPLICANT: Vojdani, Aristo
; TITLE OF INVENTION: IDENTIFICATION OF ETIOLOGY OF AUTISM
; FILE REFERENCE: IMSCI2.008A
; CURRENT APPLICATION NUMBER: US/10/770,712
; CURRENT FILING DATE: 2004-02-03
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically prepared peptide sequence
US-10-770-712-6

Query Match      100.0%; Score 94; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ENPVVHFFKNIVTPRTP 17
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Db      1 ENPVVHFFKNIIVTRTP 17
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RESULT 7
US-09-740-003-2
; Sequence 2, Application US/09740003
; Publication No. US20020039562A1
; GENERAL INFORMATION:
; APPLICANT: RAYCHAUDHURI, SYAMAL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: BLACK, AMELIA
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
; FILE REFERENCE: 37003/275802
; CURRENT APPLICATION NUMBER: US/09/740,003
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/024,220
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 08/476,674
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/351,001
; PRIOR FILING DATE: 1994-12-07
; PRIOR APPLICATION NUMBER: 08/319,787
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 07/735,069
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-740-003-2
Query Match      100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIIVTRTP 17
|||||
Db      2 ENPVVHFFKNIIVTRTP 18
|||||
RESULT 8
US-09-768-872-1
; Sequence 1, Application US/09768872
; Patent No. US2002005466A1
; GENERAL INFORMATION:
; APPLICANT: Aharoni, Rina
; APPLICANT: Teitelbaum, Dvora
; APPLICANT: Arnon, Ruth
; APPLICANT: Sela, Michael
; APPLICANT: Fridkis-Hareli, Masha
; APPLICANT: Strominger, Jack
; TITLE OF INVENTION: Treatment of Autoimmune Conditions with Copolymer 1
; FILE REFERENCE: 1662/493762
; CURRENT APPLICATION NUMBER: US/09/768,872
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/093,859
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 60/101,825
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: US 60/102,960
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 60/106,350
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 60/108,184
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/123,675

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; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (MBP residues 84-102)
US-09-768-872-1
Query Match      100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENPVVHFFKNIIVTRTP 17
|||||
Db      2 ENPVVHFFKNIIVTRTP 18
|||||
RESULT 9
US-09-766-378A-32
; Sequence 32, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jin-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,378A
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,190
; FILING DATE: 29-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Corleiss, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-766-378A-32
Query Match      100.0%; Score 94; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 2 ENPVVHFFKNIIVTRTP 18
| | | | | | | | | | | | | | | | | | | | |

RESULT 10

US-10-239-313A-143
; Sequence 143, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-143

Query Match 100.0%; Score 94; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | |

RESULT 11

US-10-743-398-2
; Sequence 2, Application US/10743398
; Publication No. US20040197331A1
; GENERAL INFORMATION:
; APPLICANT: RAYCHAUDHURI, SYAMAL
; APPLICANT: RASTETTER, WILLIAM H.
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
; FILE REFERENCE: 37003/307430
; CURRENT APPLICATION NUMBER: US/10/743,398
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 09/740,003
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/024,220
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 08/476,674
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/351,001
; PRIOR FILING DATE: 1994-12-07
; PRIOR APPLICATION NUMBER: 08/919,787
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 07/735,069
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-743-398-2

Query Match 100.0%; Score 94; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 2 ENPVVHFFKNIIVTRTP 18
| | | | | | | | | | | | | | | | | | | | |

RESULT 12

US-09-766-378A-28
; Sequence 28, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; Acevedo, Jorge
; Burkhardt, Martin
; Jiao, Jin-an
; Wong, Jing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dikey, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/766,378A
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,190
; FILING DATE: 29-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-766-378A-28

Query Match 100.0%; Score 94; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 3 ENPVVHFFKNIIVTRTP 19
| | | | | | | | | | | | | | | | | | | | |

RESULT 13

US-09-836-433-30
 ; Sequence 30, Application US/09836433
 ; Publication No. US20030049797A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yuki, Yoshikazu
 ; APPLICANT: Uda, Shigeo
 ; TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
 ; FILE REFERENCE: No. US20030049797A1 Assigned
 ; CURRENT APPLICATION NUMBER: US/09/836,433
 ; CURRENT FILING DATE: 2001-04-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 30
 ; TYPE: PRT
 ; ORGANISM: synthetic construct
 ; US-09-836-433-30

Query Match 100.0%; Score 94; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTPRTP 17
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 Db 3 ENPVVHFFKNIIVTPRTP 19

RESULT 14

US-09-859-012-35
 ; Sequence 35, Application US/09859012
 ; Publication No. US20040253632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODE, PETER
 ; APPLICANT: WITTMAN, VAUGHAN
 ; APPLICANT: WEIDANZ, JON A.
 ; APPLICANT: BURKHARDT, MARTIN
 ; APPLICANT: CARD, KIMBERLYN F.
 ; APPLICANT: TAL, RONY
 ; APPLICANT: ACEVEDO, JORGE
 ; APPLICANT: WONG, HING C.
 ; TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS
 ; FILE REFERENCE: 49444 (71758)
 ; CURRENT APPLICATION NUMBER: US/09/859,012
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 60/206,920
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; TYPE: PRT
 ; LENGTH: 20
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
 ; OTHER INFORMATION: peptide

US-09-859-012-35
 ; Sequence 35, Application US/09859012
 ; Publication No. US20040253632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODE, PETER
 ; APPLICANT: WITTMAN, VAUGHAN

Query Match 100.0%; Score 94; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTPRTP 17
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 Db 3 ENPVVHFFKNIIVTPRTP 19

RESULT 15

US-09-859-012-49
 ; Sequence 49, Application US/09859012
 ; Publication No. US20040253632A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RHODE, PETER
 ; APPLICANT: WITTMAN, VAUGHAN

; APPLICANT: WEIDANZ, JON A.
 ; APPLICANT: BURKHARDT, MARTIN
 ; APPLICANT: CARD, KIMBERLYN F.
 ; APPLICANT: TAL, RONY
 ; APPLICANT: ACEVEDO, JORGE
 ; APPLICANT: WONG, HING C.
 ; TITLE OF INVENTION: MODULATION OF T CELL RECEPTOR INTERACTIONS
 ; FILE REFERENCE: 49444 (71758)
 ; CURRENT APPLICATION NUMBER: US/09/859,012
 ; CURRENT FILING DATE: 2001-05-16
 ; PRIOR APPLICATION NUMBER: 60/206,920
 ; PRIOR FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 49
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-859-012-49

Query Match 100.0%; Score 94; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTPRTP 17
 |||||
 Db 3 ENPVVHFFKNIIVTPRTP 19

Search completed: February 22, 2006, 22:03:10
 Job time : 9.69085 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:37:34 ; Search time 2.52504 Seconds
(without alignments)
556.619 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFFKNIIVTRTP 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	2	US-09-137-759-3
2	94	100.0	17	2	US-09-378-244-3
3	94	100.0	18	1	US-08-468-540B-18
4	94	100.0	19	1	US-08-640-344-2
5	94	100.0	19	1	US-08-468-540B-9
6	94	100.0	19	1	US-08-468-540B-17
7	94	100.0	19	1	US-08-468-540B-24
8	94	100.0	19	2	US-08-297-395-1
9	94	100.0	19	2	US-09-024-220-2
10	94	100.0	19	2	US-08-960-190A-32
11	94	100.0	19	2	US-08-449-728-2
12	94	100.0	19	2	US-09-077-028A-15
13	94	100.0	19	2	US-09-740-003-2
14	94	100.0	20	1	US-08-640-344-1
15	94	100.0	20	1	US-08-640-344-3
16	94	100.0	20	1	US-08-640-344-4
17	94	100.0	20	1	US-08-640-344-5
18	94	100.0	20	1	US-08-640-344-6
19	94	100.0	20	1	US-08-640-344-7
20	94	100.0	20	2	US-08-960-190A-28
21	94	100.0	23	1	US-08-787-547-1
22	94	100.0	24	1	US-08-480-190-46
23	94	100.0	24	1	US-08-488-379-46
24	94	100.0	24	2	US-08-475-399A-46
25	94	100.0	24	2	US-09-239-043D-2501
26	94	100.0	24	2	US-08-077-255A-46
27	94	100.0	24	4	PCT-US93-07545-46

28	94	100.0	40	2	US-08-297-395-2	Sequence 2, Appli
29	94	100.0	168	6	5194425-4	Patent No. 5194425
30	94	100.0	170	1	US-08-227-372-1	Sequence 1, Appli
31	94	100.0	170	1	US-08-327-357A-1	Sequence 1, Appli
32	94	100.0	170	2	US-08-470-397-1	Sequence 1, Appli
33	94	100.0	170	2	US-09-007-520-1	Sequence 3, Appli
34	94	100.0	170	2	US-08-462-351-3	Sequence 1, Appli
35	94	100.0	170	2	US-09-055-263-1	Sequence 3, Appli
36	94	100.0	170	2	US-09-007-520-1	Sequence 1, Appli
37	94	100.0	170	2	US-08-342-408B-2	Sequence 2, Appli
38	94	100.0	170	2	US-09-602-807-3	Sequence 3, Appli
39	94	100.0	170	6	5194425-3	Patent No. 5194425
40	94	100.0	171	1	US-08-781-122-2	Sequence 2, Appli
41	94	100.0	171	2	US-09-137-759-2	Sequence 2, Appli
42	94	100.0	171	2	US-08-953-937-2	Sequence 2, Appli
43	94	100.0	171	2	US-09-378-244-2	Sequence 2, Appli
44	94	100.0	171	2	US-09-989-476-2	Sequence 2, Appli
45	94	100.0	171	2	US-10-270-707-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-137-759-3
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; CURRENT FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-137-759-3

Query Match 100.0%; Score 94; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
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Db 1 ENPVVHFFKNIIVTRTP 17

RESULT 2

US-09-378-244-3
; Sequence 3, Application US/09378244
; Patent No. 6379670
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN
; FILE REFERENCE: 690068.405C2
; CURRENT APPLICATION NUMBER: US/09/378,244
; CURRENT FILING DATE: 1999-08-19

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-378-244-3

Query Match      100.0%; Score 94; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17
Db 1 ENPVVHFFKNIVTPRP 17

RESULT 3
US-08-468-540B-18
; Sequence 18, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-18

Query Match      100.0%; Score 94; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17

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Db 1 ENPVVHFFKNIVTPRP 17

RESULT 4
US-08-640-344-2
; Sequence 2, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKKU, PRABHA
; APPLICANT: DESHPANDE, SHRIRAM
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-640-344-2

Query Match      100.0%; Score 94; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRP 17
Db 2 ENPVVHFFKNIVTPRP 18

RESULT 5
US-08-468-540B-9
; Sequence 9, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY

```

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; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-9

Query Match 100.0%; Score 94; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 6
US-08-468-540B-17
; Sequence 17, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-24

Query Match 100.0%; Score 94; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-17

Query Match 100.0%; Score 94; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 7
US-08-468-540B-24
; Sequence 24, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-24

Query Match 100.0%; Score 94; DB 1; Length 19;

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Best Local Similarity 100.0%; Pred. No. 8e-09; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
Db 2 ENPVVHFFKNIIVTRTP 18

RESULT 8

US-08-297-395-1
; Sequence 1, Application US/08297395A
; Patent No. 6039947
; GENERAL INFORMATION:
; APPLICANT: Howard L. Weiner
; APPLICANT: David A. Hafler
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
; TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
; FILE REFERENCE: 1010/05723US3
; CURRENT APPLICATION NUMBER: US/08/297.395A
; CURRENT FILING DATE: 1994-08-11
; EARLIER APPLICATION NUMBER: 08/059,189
; EARLIER FILING DATE: 1993-05-06
; EARLIER APPLICATION NUMBER: 07/502,559
; EARLIER FILING DATE: 1990-03-30
; EARLIER APPLICATION NUMBER: PCT/US88/02139
; EARLIER FILING DATE: 1988-06-24
; EARLIER APPLICATION NUMBER: 07/065,734
; EARLIER FILING DATE: 1987-06-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-297-395-1

Query Match 100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
Db 2 ENPVVHFFKNIIVTRTP 18

RESULT 9

US-09-024-220-2
; Sequence 2, Application US/09024220
; Patent No. 6197311
; GENERAL INFORMATION:
; APPLICANT: RAYCHAUDHURI, Syamal
; APPLICANT: RASTETTER, William H.
; APPLICANT: BLACK, Amelia
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE
; RESPONSES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,220
; FILING DATE: 17-Feb-1998
; CLASSIFICATION: <Unknown>
; TELEPHONE: 24-JUL-1999

25-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,674
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/919,787
FILING DATE: 24-JUL-1992
APPLICATION NUMBER: US 07/735,069
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-024-220-2

Query Match 100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
Db 2 ENPVVHFFKNIIVTRTP 18

RESULT 10

US-08-960-190A-32
; Sequence 32, Application US/08960190A
; Patent No. 6232445
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; APPLICANT: Acevedo, Jorge
; APPLICANT: Burkhardt, Martin
; APPLICANT: Jiao, Jin-an
; APPLICANT: Wong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,190A
; FILING DATE: 29-OCT-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440

```

;
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-960-190A-32

Query Match      100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
   |||||
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 11
US-08-449-728-2
; Sequence 2, Application US/08449728
; Patent No. 6270769
; GENERAL INFORMATION:
; APPLICANT: SYAMAL RAYCHAUDHURI
; APPLICANT: WILLIAM H. RASTETTER
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC
; TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,728
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/735,069
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 194/160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-449-728-2

Query Match      100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
   |||||
Db 2 ENPVVHFFKNIVTPRTP 18

;
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-077-028A-15

Query Match      100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
   |||||
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 12
US-09-077-028A-15
; Sequence 15, Application US/09077028A
; Patent No. 6531133
; GENERAL INFORMATION:
; APPLICANT: HAYA LOREBERBOUM-GALSKI
; APPLICANT: IDA STEINBERGER
; APPLICANT: EVELINE BEAUD
; APPLICANT: IRINA MARIANOVSKY
; APPLICANT: SHAI YARKONI
; TITLE OF INVENTION: PSEUDOMONAS EXOTOXIN-MYELIN BASIC PROTEIN CHIMERIC
; FILE REFERENCE: LOREBERBOUM-1
; CURRENT APPLICATION NUMBER: US/09/077,028A
; CURRENT FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: IL116044
; PRIOR FILING DATE: 1995-11-17
; PRIOR APPLICATION NUMBER: IL116559
; PRIOR FILING DATE: 1995-12-26
; PRIOR APPLICATION NUMBER: PCT/IL96/00151
; PRIOR FILING DATE: 1996-11-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-077-028A-15

Query Match      100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
   |||||
Db 2 ENPVVHFFKNIVTPRTP 18

RESULT 13
US-09-740-003-2
; Sequence 2, Application US/09740003
; Patent No. 6733763
; GENERAL INFORMATION:
; APPLICANT: RAYCHAUDHURI, SYAMAL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: BLACK, AMELIA
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE RESPONSES
; FILE REFERENCE: 37003/275802
; CURRENT APPLICATION NUMBER: US/09/740,003
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/024,220
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 08/476,674
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/351,001
; PRIOR FILING DATE: 1994-12-07
; PRIOR APPLICATION NUMBER: 08/919,787
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 07/735,069
; PRIOR FILING DATE: 1991-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-09-740-003-2

Query Match      100.0%; Score 94; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ENPVVHFFKNIIVTRTP 17
 Db 2 ENPVVHFFKNIIVTRTP 18

RESULT 14

US-08-640-344-1
 ; Sequence 1, Application US/08640344
 ; Patent No. 5824315
 ; GENERAL INFORMATION:
 ; APPLICANT: NAG, BISHWAJIT
 ; APPLICANT: MUKKU, PRABHA
 ; APPLICANT: DESHPANDE, SHRIKANT
 ; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
 ; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
 ; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: U.S.A.
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/640,344
 ; FILING DATE: 30-APR-1996
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STORELLA ESQ., JOHN R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 14058-004800
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-640-344-1

Query Match 100.0%; Score 94; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
 Db 3 ENPVVHFFKNIIVTRTP 19

RESULT 15

US-08-640-344-3
 ; Sequence 3, Application US/08640344
 ; Patent No. 5824315
 ; GENERAL INFORMATION:
 ; APPLICANT: NAG, BISHWAJIT
 ; APPLICANT: MUKKU, PRABHA
 ; APPLICANT: DESHPANDE, SHRIKANT
 ; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
 ; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
 ; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
 ; CITY: SAN FRANCISCO

; STATE: CALIFORNIA
 ; COUNTRY: U.S.A.
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/08/640,344
 ; FILING DATE: 30-APR-1996
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STORELLA ESQ., JOHN R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 14058-004800
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-640-344-3

Query Match 100.0%; Score 94; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIIVTRTP 17
 Db 3 ENPVVHFFKNIIVTRTP 19

Search completed: February 22, 2006, 21:39:50
 Job time : 3.52504 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: February 22, 2006, 21:24:24 ; Search time 11.304 Seconds
(without alignments)
1061.041 Million cell updates/sec

Title: US-10-000-439-13
Perfect score: 94
Sequence: 1 ENPVVHFFKNIVTPRTP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	74	2 Q6AI64 HUMAN	Q6ai64 homo sapien
2	94	100.0	128	2 Q505J1 RAT	Q505j1 rattus norv
3	94	100.0	150	2 Q5NVG4 PONPY	Q5nvq4 pongo pygma
4	94	100.0	154	2 Q542T4 MOUSE	Q542t4 mus musculu
5	94	100.0	158	2 Q8R4K6 RAT	Q8r4k6 rattus norv
6	94	100.0	160	2 Q6FI04 HUMAN	Q6fi04 homo sapien
7	94	100.0	160	2 Q6FH37 HUMAN	Q6fh37 homo sapien
8	94	100.0	160	2 Q5R7J4 PONPY	Q5r7j4 pongo pygma
9	94	100.0	167	1 MBP_CAVPO	P25188 cavia porce
10	94	100.0	168	1 MBP_RABIT	P25274 oryctolagus
11	94	100.0	169	1 MBP_BOVIN	P02887 bos taurus
12	94	100.0	171	1 MBP_PANTR	P06906 pan troglod
13	94	100.0	171	1 MBP_PIG	P81558 sus scrofa
14	94	100.0	171	2 Q5R618 PONPY	Q5r618 pongo pygma
15	94	100.0	173	2 Q6J2R3 PIG	Q6j2r3 sus scrofa
16	94	100.0	180	2 Q6PK23 HUMAN	Q6pk23 homo sapien
17	94	100.0	194	1 MBP_RAT	P02888 rattus norv
18	94	100.0	203	2 Q65ZS4 HUMAN	Q65zs4 homo sapien
19	94	100.0	250	1 MBP_MOUSE	P04370 mus musculu
20	94	100.0	304	1 MBP_HUMAN	P02686 homo sapien
21	87	92.6	173	1 MBP_CHICK	P15720 gallus gall
22	87	92.6	178	2 Q511E1 GEGJA	Q511e1 gekko japon
23	87	92.6	178	2 Q569T2 XENLA	Q569t2 xenopus lae
24	84	89.4	175	1 MBP_XENLA	P87346 xenopus lae
25	78	83.0	172	1 MBP_HORSE	P83487 equus cabal
26	65	69.1	217	2 Q4RF19 TETNG	Q4rf19 tetraodon n
27	61	64.9	154	1 MBP_RAJER	Q91325 raja erinac
28	61	64.9	154	1 MBP_SQUAC	Q91439 squalus aca
29	60	63.8	128	1 MBP_CAROB	P98190 carachinu
30	53	56.4	154	1 MBP_HETFR	P20939 heterodonu
31	52	55.3	88	2 Q512C7 BRARE	Q512c7 brachydanio

32	51	54.3	516	2 Q5WTL4 LEGPL	Q5wtl4 legionella
33	49.5	52.7	668	2 Q86I29 DICDI	Q86i29 dictyosteli
34	49	52.1	516	2 Q5XIV3 LEGPA	Q5xiv3 legionella
35	47	50.0	300	2 Q833W5 ENTEFA	Q833w5 enterococcu
36	47	50.0	516	2 Q5ZSD2 LEGPH	Q5zsd2 legionella
37	47	50.0	669	2 Q6D8B7 ERWCT	Q6d8b7 erwinia car
38	46	48.9	233	2 Q6J37 CAEABR	Q6j37 caenorhabdi
39	46	48.9	287	2 Q5SM89 9CAUD	Q5sm89 cyanophage
40	46	48.9	439	2 Q4ZST7 PSESY	Q4zst7 pseudomonas
41	46	48.9	440	2 Q881D3 PSESM	Q881d3 pseudomonas
42	46	48.9	888	2 Q4QAJ6 LEIMA	Q4qaj6 leishmania
43	46	48.9	1529	2 Q7ZX12 XENLA	Q7zx12 xenopus lae
44	45	47.9	308	1 Y1128 METJA	Q58528 methanococc
45	45	47.9	315	2 Q4H5F9 9DEIO	Q4h5f9 deinococcus

ALIGNMENTS

RESULT 1
Q6AI64 HUMAN
ID Q6AI64_HUMAN PRELIMINARY; PRT; 74 AA.
AC Q6AI64;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Hypothetical protein DKFZp686I0845 (Fragment).
GN Name=DKFZp686I0845;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Amygdala;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiipp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR627018; CH10359.1; -; mRNA.
DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
DR InterPro; IPR000548; Myelin_MBP.
DR Pfam; PF01669; Myelin_MBP; 1.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Hypothetical protein.
FT NON_TER 74 74
SQ SEQUENCE 74 AA; 8265 MW; ACFE96ACBB9AE551 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
|||||
DB 41 ENPVVHFFKNIVTPRTP 57

RESULT 2
Q505J1 RAT
ID Q505J1_RAT PRELIMINARY; PRT; 128 AA.
AC Q505J1;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE Myelin basic protein.
GN Name=Mbp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vllalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP NUCLEOTIDE SEQUENCE.
 RC NIH MGC Project;
 RG TISSUE=Brain;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC094522; AAH94522.1; -; mRNA.
 DR InterPro: IPR000548; Myelin BP.
 DR Pfam: PF01669; Myelin MBP; I.
 DR PRINTS; PR00212; MYELINMBP.
 DR ProDom; PD004542; Myelin BP; 1.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 SQ SEQUENCE 128 AA; 14211 MW; 2DAF033C19CF111C CRC64;

Query Match 100.0%; Score 94; DB 2; Length 128;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0;

QY 1 ENPVVHFFKNIVTPRT 17
 DB 81 ENPVVHFFKNIVTPRT 97
 |||||
 |||||

RESULT 3
 Q5NVG4 PONPY PRELIMINARY; PRT; 150 AA.
 AC Q5NVG4
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE Hypothetical protein DKFZp459G2410.
 GN Name=DKFZp459G2410;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OX NCBI_TaxID=9660;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Cortex;
 RC The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR926072; CAI29699.1; -; mRNA.
 DR GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
 DR InterPro; IPR000548; Myelin BP.
 DR Pfam; PF01669; Myelin MBP; I.
 DR PRINTS; PR00212; MYELINMBP.
 DR ProDom; PD004542; Myelin BP; 1.

DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 150 AA; 16277 MW; AF41CDB96D8FD01 CRC64;
 Query Match 100.0%; Score 94; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
 DB 63 ENPVVHFFKNIVTPRT 79
 |||||
 |||||

RESULT 4
 Q542T4 MOUSE PRELIMINARY; PRT; 154 AA.
 AC Q542T4
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Adult male spinal cord cDNA, RIKEN full-length enriched library,
 DE clone:A330075E24 product:myelin basic protein, full insert
 DE sequence.
 DE Name=Mbp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44(1999).
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=21085660; PubMed=1217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Spinal cord;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragan T.A., Fletcher C., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Query Match 100.0%; Score 94; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 84 ENPVVHFFKNIIVTRTP 100

RESULT 7
 Q6FH37 HUMAN
 ID Q6FH37 HUMAN PRELIMINARY; PRT; 160 AA.
 AC Q6FH37;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE MBP protein (Fragment).
 GN Name=MBP;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., LaBaer J.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR541919; CAG46717.1; -, mRNA.
 FT NON TER 160
 SQ SEQUENCE 160 AA; 17343 MW; 0107AAD603FCD876 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 84 ENPVVHFFKNIIVTRTP 100

RESULT 8
 Q5R7J4 PONPY
 ID Q5R7J4 PONPY PRELIMINARY; PRT; 160 AA.
 AC Q5R7J4;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein DKFZp459C0311.
 GN Name=DKFZp459C0311;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeinger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR860121; CAH92286.1; -, mRNA.
 GO GO:0019911; F:structural constituent of myelin sheath; IEA.
 DR InterPro; IPR000548; Myelin BP.
 DR Pfam; PF01669; Myelin MBP; I.
 DR PRINTS; PR00212; MYELINMBP.
 DR ProDom; PD004542; Myelin BP; 1.
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 160 AA; 17317 MW; 1A0601CCB257D9C6 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
 |||||
 DB 84 ENPVVHFFKNIIVTRTP 100

RESULT 9
 MBP_CAVPO
 ID MBP_CAVPO STANDARD; PRT; 167 AA.
 AC P25188;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Myelin basic protein (MBP).
 GN Name=MBP;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA MEDLINE=84215086; PubMed=6202840;
 RA Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
 RT "Sequence of guinea pig myelin basic protein.";
 RL J. Neurochem. 43:100-105 (1984).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 7-156.
 RC STRAIN=Hartley; TISSUE=Spinal cord;
 RA Kim G., Tanuma N., Matsumoto Y.;
 RT "DNA vaccination using Guinea pig myelin basic protein coding region
 in experimental autoimmune encephalomyelitis.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP PROTEIN SEQUENCE OF 45-87.
 RA Shapira R., McKneally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640 (1971).
 RN [4]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=76025020; PubMed=51849;
 RA Deibler G.E., Martenson R.E., Kramer A.J., Kies M.W.;
 RT "The contribution of phosphorylation and loss of COOH-terminal
 arginine to the microheterogeneity of myelin basic protein.";
 RL J. Biol. Chem. 250:7931-7938 (1975).
 CC -I- FUNCTION: Is, with PLP, the most abundant protein component of the
 myelin membrane in the CNS. Has a role in both the formation and
 stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 function in the assembly of an optimized, biochemically functional
 myelin membrane (By similarity).
 CC -I- SUBUNIT: Homodimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -I- TISSUE SPECIFICITY: Found in both the central and the peripheral
 nervous system.
 CC -I- PTM: At least 5 charge isomers; C1 (the most cationic, least
 modified, and most abundant form), C2, C3, C4 and C5 (the least
 cationic form); are produced as a result of optional
 posttranslational modifications such as phosphorylation of serine
 or threonine residues, deamidation of glutamine or asparagine
 residues, citrullination and methylation of arginine residues. C1
 and C2 are unphosphorylated, C3 and C4 are monophosphorylated and
 C5 is phosphorylated at two positions.
 CC -I- SIMILARITY: Belongs to the myelin basic protein family.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
DR EMBL; AF074337; AAC26130.1; -; mRNA.
DR PIR; A37246; A37246.
DR HSSP; P02686; IQCL.
DR InterPro; IPR000548; Myelin_BP.
DR PANTHER; PTHR11429; Myelin_MBP; 1.
DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR ProDom; PD004542; Myelin_MBP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Acetylation; Autoimmune encephalomyelitis; Citrullination;
KW Direct protein sequencing; Methylation; Myelin; Phosphorylation;
KW Structural protein.
FT REGION 45 87
FT Induces experimental autoimmune
FT encephalomyelitis (EAE) 1.
FT Induces experimental autoimmune
FT encephalomyelitis (EAE) 2.
FT REGION 114 122
FT MOD_RES 1 1
FT MOD_RES 7 7
FT MOD_RES 12 12
FT MOD_RES 25 25
FT MOD_RES 31 31
FT MOD_RES 56 56
FT MOD_RES 71 71
FT MOD_RES 97 97
FT MOD_RES 102 102
FT MOD_RES 106 106
FT MOD_RES 114 114
FT MOD_RES 129 129
FT MOD_RES 144 144
FT MOD_RES 156 156
FT MOD_RES 158 158
FT MOD_RES 162 162
FT MOD_RES 167 167
FT MOD_RES 167 AA; 18213 MW; 866D31F1ESACFEAG CRC64;
SQ SEQUENCE 167 AA; 18213 MW; 866D31F1ESACFEAG CRC64;

Query Match 100.0%; Score 94; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRT 17
Db 82 ENPVVHFFKNIVTPRT 98

RESULT 10
MBP_RABIT STANDARD; PRT; 168 AA.
AC P25774;
DT 01-MAY-1992 (Rel. 22, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Myelin basic protein (MBP) (Myelin A1 protein) (Myelin P1 protein).
GN Name=MBP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PRELIMINARY PROTEIN SEQUENCE.
RC TISSUE=Sciatic nerve;
RX MEDLINE=73190037; PubMed=4662101;
RA Brostoff S.W., Eylar E.H.;
RT "The proposed amino acid sequence of the P1 protein of rabbit sciatic
RT nerve myelin.";
RL Arch. Biochem. Biophys. 153:590-598 (1972).
RN [2]
RP PROTEIN SEQUENCE OF 45-86.

```

```

RA Shapira R., McKneally S.S., Chou F., Kibler R.F.;
RT "Encephalogenic fragment of myelin basic protein. Amino acid
RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
RL J. Biol. Chem. 246:4630-4640 (1971).
RN [3]
RP PHOSPHORYLATION.
RX MEDLINE=83108902; PubMed=6185481;
RA Martenson R.E., Law M.J., Deibler G.E.;
RT "Identification of multiple in vivo phosphorylation sites in rabbit
RT myelin basic protein.";
RL J. Biol. Chem. 258:930-937 (1983).
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- TISSUE SPECIFICITY: Found in both the central and the peripheral
CC nervous system.
CC -!- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Belongs to the myelin basic protein family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P02686; IQCL.
CC InterPro; IPR000548; Myelin_BP.
CC PANTHER; PTHR11429; Myelin_BP; 1.
CC Pfam; PF01669; Myelin_MBP; 1.
CC PRINTS; PR00212; MYELINMBP.
CC ProDom; PD004542; Myelin_BP; 1.
CC ProDom; PD004542; Myelin_MBP; 1.
CC PROSITE; PS00569; MYELIN_MBP; 1.
KW Acetylation; Autoimmune encephalomyelitis; Citrullination;
KW Direct protein sequencing; Methylation; Myelin; Phosphorylation;
KW Structural protein.
FT REGION 45 86
FT Induces experimental autoimmune
FT encephalomyelitis (EAE).
FT N-acetylalanine (Probable).
FT MOD_RES 1 1
FT MOD_RES 7 7
FT MOD_RES 12 12
FT MOD_RES 25 25
FT MOD_RES 31 31
FT MOD_RES 56 56
FT MOD_RES 69 69
FT MOD_RES 96 96
FT MOD_RES 101 101
FT MOD_RES 105 105
FT MOD_RES 105 105
FT MOD_RES 113 113
FT MOD_RES 128 128
FT MOD_RES 145 145
FT MOD_RES 157 157
FT MOD_RES 159 159
FT MOD_RES 163 163
FT MOD_RES 168 168
FT MOD_RES 168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;
FT CONFLICT 46
FT S -> G (in Ref. 2).
SQ SEQUENCE 168 AA; 18217 MW; EC3C97ACD2C08EA6 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ENPVVHFFKNIIVTRTP 17
 Db 81 ENPVVHFFKNIIVTRTP 97

RESULT 11
 MBP_BOVIN STANDARD; PRT; 169 AA.
 AC P02687; Q9BGM8; Q9TS63; Q9TS66;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-SEP-2005 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa microtubule
 DE stabilizing protein).
 GN Name=MBP;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RX MEDLINE=72007306; PubMed=5096093;
 RA Eylar E.H., Brostoff S.W., Hashim G., Caccam J., Burnett P.;
 RT "Basic A1 protein of the myelin membrane. The complete amino acid
 RT sequence.";
 RL J. Biol. Chem. 246:5770-5784 (1971).
 RN [2]
 RP SEQUENCE REVISION.
 RX MEDLINE=74070688; PubMed=4129204;
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";
 RL J. Biol. Chem. 249:559-567 (1974).
 RN [3]
 RP NUCLEOTIDE SEQUENCE OF 4-56.
 RA Pietrowski D., Medugorac I., Foerster M.;
 RT "A new MBP allele in Bos taurus is characterized by BseNI PCR-RFLP.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.
 RN [4]
 RP PROTEIN SEQUENCE OF 43-87.
 RA Shapira R., McKneally S.S., Chou F.C.-H., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640 (1971).
 RN [5]
 RP PROTEIN SEQUENCE OF 38-58 AND 119-141.
 RC TISSUE=Brain;
 RX MEDLINE=93003019; PubMed=1382581;
 RA Pirollet F., Derancourt J., Haiech J., Job D., Margolis R.L.;
 RT "Ca(2+)-calmodulin regulated effectors of microtubule stability in
 RT bovine brain.";
 RL Biochemistry 31:8849-8855 (1992).
 RN [6]
 RP PROTEIN SEQUENCE OF 30-42; 74-89 AND 114-129.
 RX MEDLINE=96107211; PubMed=8530487; DOI=10.1074/jbc.270.51.30551;
 RA Prasad K., Barouch W., Martin B.M., Greene L.E., Eisenberg E.;
 RT "Purification of a new clathrin assembly protein from bovine brain
 RT coated vesicles and its identification as myelin basic protein.";
 RL J. Biol. Chem. 270:30551-30556 (1995).
 RN [7]
 RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.
 RX MEDLINE=70178977; PubMed=5442707;
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;
 RT "Experimental allergic encephalomyelitis: synthesis of disease-
 RT inducing site of the basic protein.";
 RL Science 168:1220-1223 (1970).
 RN [8]
 RP METHYLATION.
 RX MEDLINE=71153946; PubMed=4994464;
 RA Brostoff S.W., Eylar E.H.;
 RT "Localization of methylated arginine in the A1 protein from myelin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769 (1971).

RN [9]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=76167591; PubMed=57115;
 RA Chou F.C.-H., Chou C.-H.J., Shapira R., Kibler R.F.;
 RT "Basis of microheterogeneity of myelin basic protein.";
 RL J. Biol. Chem. 251:2671-2679 (1976).
 RN [10]
 RP PROTEIN SEQUENCE OF 97-104, AND PHOSPHORYLATION SITE THR-97.
 RX MEDLINE=91060584; PubMed=1700979;
 RA Erickson A.K., Payne D.M., Martino P.A., Rossomando A.J.,
 RA Shabanowitz J., Weber M.J., Hunt D.F., Scargill T.W.;
 RT "Identification by mass spectrometry of threonine 97 in bovine myelin
 RT basic protein as a specific phosphorylation site for mitogen-activated
 RT protein kinase.";
 RL J. Biol. Chem. 265:19728-19735 (1990).
 RN [11]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=98153125; PubMed=9485392; DOI=10.1021/bi972347t;
 RA Zand R., Li M.X., Jin X., Lubman D.;
 RT "Determination of the sites of posttranslational modifications in the
 RT charge isomers of bovine myelin basic protein by capillary
 RT electrophoresis-mass spectroscopy.";
 RL Biochemistry 37:2441-2449 (1998).
 RN [12]
 RP DIMERIZATION.
 RX MEDLINE=80198320; PubMed=6155143;
 RA Smith R.;
 RT "Sedimentation analysis of the self-association of bovine myelin basic
 RT protein.";
 RL Biochemistry 19:1826-1831 (1980).
 CC -1- FUNCTION: Is, with PLP, the most abundant protein component of the
 CC myelin membrane in the CNS. Has a role in both the formation and
 CC stabilization of this compact multilayer arrangement of bilayers.
 CC Each splice variant and charge isomer may have a specialized
 CC function in the assembly of an optimized, biochemically functional
 CC myelin membrane (By similarity).
 CC -1- SUBUNIT: Homodimer; self-associates in the presence of lysolipid.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
 CC -1- TISSUE SPECIFICITY: Found in both the central and the peripheral
 CC nervous system.
 CC -1- PTM: At least 6 charge isomers; C1 (the most cationic and least
 CC modified form), C2, C3, C4, C5 and C6 (the least cationic form);
 CC are produced as a result of optional posttranslational
 CC modifications, such as phosphorylation of serine or threonine
 CC residues, deamidation of glutamine or asparagine residues,
 CC citrullination and methylation of arginine residues.
 CC -1- SIMILARITY: Belongs to the myelin basic protein family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

EMBL: AF226693; AAK00645.1; -; mRNA.
 PIR: A92089; MBBOB.
 HSSP: P02686; IQCU.
 InterPro: IPR000548; Myelin_BP.
 PANTHER: PTHR11429; Myelin_BP; 1.
 Pfam: PF01669; Myelin_MBP; 1.
 PRINTS: PR00212; MYELINMBP.
 ProDom: PD004542; Myelin_BP; 1.
 PROSITE: PS00569; MYELIN_MBP; 1.
 Acetylation; Autoimmune encephalomyelitis; Citrullination;
 Direct protein sequencing; Methylation; Myelin; Phosphorylation;
 Structural protein.
 REGION 43 87 Induces experimental autoimmune
 encephalomyelitis (EAE) 1.
 REGION 114 122 Induces experimental autoimmune
 encephalomyelitis (EAE) 2.
 FT MOD_RES 1 1 N-acetylalanine.
 FT MOD_RES 7 7 Phosphoserine (in C5 and C6).
 FT MOD_RES 10 10 Phosphoserine (By similarity).

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FT MOD_RES 23 23 Citrulline (By similarity).
FT MOD_RES 29 29 Citrulline (By similarity).
FT MOD_RES 54 54 Phosphoserine (in C4, C5 and C6).
FT MOD_RES 69 69 Phosphoserine (By similarity).
FT MOD_RES 97 97 Phosphothreonine (by MAPK) (in C3, C4, C5
and C6).
FT MOD_RES 102 102 Deamidated glutamine (in form C5).
FT MOD_RES 106 106 Omega-N-methylarginine (alternate).
FT MOD_RES 106 106 Symmetric dimethylarginine (alternate).
FT MOD_RES 114 114 Phosphoserine (By similarity).
FT MOD_RES 129 129 Citrulline (By similarity).
FT MOD_RES 146 146 Deamidated glutamine (in form C2).
FT MOD_RES 158 158 Citrulline (By similarity).
FT MOD_RES 160 160 Phosphoserine (in C4 and C6).
FT MOD_RES 164 164 Phosphoserine (in C3, C5 and C6).
FT MOD_RES 169 169 Citrulline (Probable).
SQ SEQUENCE 169 AA; 18323 MW; 8E1157B7A1978484 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 12
MBP_PANTH
ID MBP_PANTH STANDARD; PRT; 171 AA.
AC P06906;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Myelin basic protein (MBP).
GN Name=MBP;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP PRELIMINARY PROTEIN SEQUENCE.
RX MEDLINE=76009821; PubMed=51459; DOI=10.1016/0024-3205(75)90506-8;
RA Westall F.C., Thompson M., Kalter S.S.;
RT "The proposed sequence of the encephalitogenic protein from chimpanzee
brain".
RL Life Sci. 17:219-223(1975).
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as
CC phosphorylation of serine or threonine residues, deamidation of
CC glutamine or asparagine residues, citrullination and methylation
CC of arginine residues.
CC -!- SIMILARITY: Belongs to the myelin basic protein family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A01139; MRC2B.
DR HSP; P02686; LQCL.
DR InterPro; IPR000548; Myelin_BP.
DR PANTHER; PTHR11429; Myelin_BP; 1.

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DR Pfam; PF01669; Myelin_MBP; 1.
DR PRINTS; PD00212; MYELINMBP.
DR ProDom; PD004542; Myelin_BP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KW Acetylation; Autoimmune encephalomyelitis; Citrullination;
Direct protein sequencing; Methylation; Myelin; Phosphorylation;
KW Structural protein.
FT MOD_RES 1 1 N-acetylalanine.
FT MOD_RES 7 7 Phosphoserine (By similarity).
FT MOD_RES 12 12 Phosphoserine (By similarity).
FT MOD_RES 25 25 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 56 56 Phosphoserine (By similarity).
FT MOD_RES 71 71 Phosphoserine (By similarity).
FT MOD_RES 98 98 Phosphothreonine (By similarity).
FT MOD_RES 103 103 Deamidated glutamine (partial) (By
similarity).
FT MOD_RES 107 107 Omega-N-methylated arginine.
FT MOD_RES 115 115 Phosphoserine (By similarity).
FT MOD_RES 122 122 Citrulline (By similarity).
FT MOD_RES 130 130 Citrulline (By similarity).
FT MOD_RES 148 148 Deamidated glutamine (partial) (By
similarity).
FT MOD_RES 160 160 Citrulline (By similarity).
FT MOD_RES 162 162 Phosphoserine (By similarity).
FT MOD_RES 166 166 Phosphoserine (By similarity).
FT MOD_RES 171 171 Citrulline (By similarity).
SQ SEQUENCE 171 AA; 18560 MW; E9FED59DE6933293 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVTPRTP 17
Db 83 ENPVVHFFKNIVTPRTP 99

RESULT 13
MBP_PIG
ID MBP_PIG STANDARD; PRT; 171 AA.
AC P81558; P98189;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Myelin basic protein (MBP).
GN Name=MBP;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP PROTEIN SEQUENCE, AND METHYLATION OF ARG-107.
RC TISSUE=Brain;
RX MEDLINE=85056964; PubMed=2578056;
RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
RT "Amino acid sequence of porcine myelin basic protein.";
RL J. Neurochem. 44:134-142(1985).
RN [2]
RP ERRATUM.
RA Kira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;
RL J. Neurochem. 44:1663-1663(1985).
CC -!- FUNCTION: Is, with PLP, the most abundant protein component of the
CC myelin membrane in the CNS. Has a role in both the formation and
CC stabilization of this compact multilayer arrangement of bilayers.
CC Each splice variant and charge isomer may have a specialized
CC function in the assembly of an optimized, biochemically functional
CC myelin membrane (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic side of myelin.
CC -!- PTM: As in other animals, several charge isomers may be produced
CC as a result of optional posttranslational modifications, such as

```

phosphorylation of serine or threonine residues, deamidation of glutamine or asparagine residues, citrullination and methylation of arginine residues.
-1- SIMILARITY: Belongs to the myelin basic protein family.

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PR; A61640; MBPGB.
HSP; P02686; IQCL.
InterPro; IPR000548; Myelin_BP.
PANTHER; PTHR11429; Myelin_BP; 1.
PFam; PF01669; Myelin_MBP; 1.
PRINTS; PR00212; MYELINMBP.
ProDom; PD004542; Myelin_BP; 1.
PROSITE; PS00569; MYELIN_MBP; 1.
Myelin; Phosphorylation; Direct protein sequencing; Methylation; Acetylation; Citrullination; Structural protein.
FT MOD_RES 1 1 N-acetylalanine.
FT MOD_RES 7 7 Phosphoserine (By similarity).
FT MOD_RES 12 12 Phosphoserine (By similarity).
FT MOD_RES 25 25 Citrulline (By similarity).
FT MOD_RES 31 31 Citrulline (By similarity).
FT MOD_RES 55 55 Phosphoserine (By similarity).
FT MOD_RES 70 70 Phosphoserine (By similarity).
FT MOD_RES 98 98 Phosphothreonine (By similarity).
FT MOD_RES 103 103 Deamidated glutamine (partial) (By similarity).
FT MOD_RES 107 107 Omega-N-methylarginine (alternate).
FT MOD_RES 107 107 Symmetric dimethylarginine (alternate).
FT MOD_RES 115 115 Phosphoserine (By similarity).
FT MOD_RES 130 130 Citrulline (By similarity).
FT MOD_RES 148 148 Deamidated glutamine (partial) (By similarity).
FT MOD_RES 160 160 Citrulline (By similarity).
FT MOD_RES 162 162 Phosphoserine (By similarity).
FT MOD_RES 166 166 Phosphoserine (By similarity).
FT MOD_RES 171 171 Citrulline (By similarity).
SEQUENCE 171 AA; 18487 MW; 287ADF2F24028D9 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENPVVHFFKNIIVTPRT 17
DB 83 ENPVVHFFKNIIVTPRT 99

RESULT 14
Q5R618_PONV PRELIMINARY; PRT; 171 AA.
Q5R618;
AC 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp459C0215 (Hypothetical protein DKFZp459P2220).
GN Name=DKFZp459C0215; Synonyms=DKFZp459P2220;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo
OC NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RG Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;

Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
EMBL; CR860682; CAH92798.1; -; mRNA.
EMBL; CR926007; CAI2645.1; -; mRNA.
GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
InterPro; IPR000548; Myelin_BP.
PFam; PF01669; Myelin_MBP; 1.
PRINTS; PR00212; MYELINMBP.
ProDom; PD004542; Myelin_BP; 1.
PROSITE; PS00569; MYELIN_MBP; 1.
Hypothetical protein.
KW SEQUENCE 171 AA; 18565 MW; F8B56E03D6305540 CRC64;

Query Match 100.0%; Score 94; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENPVVHFFKNIIVTPRT 17
DB 84 ENPVVHFFKNIIVTPRT 100

RESULT 15
Q6J2R3_PIG PRELIMINARY; PRT; 173 AA.
ID Q6J2R3_PIG PRELIMINARY; PRT; 173 AA.
AC Q6J2R3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Myelin basic protein.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15771731; DOI=10.1111/j.1365-2052.2005.01236.x;
RA Kim J.G., Noneman D., Vallet J.L., Rohrer G.A., Christenson R.K.;
RT "Linkage mapping of the porcine myelin basic protein gene to chromosome 1.";
RL Anim. Genet. 36:163-164(2005).
DR EMBL; AY603684; AAT28338.1; -; mRNA.
GO; GO:0019911; F:structural constituent of myelin sheath; IEA.
InterPro; IPR000548; Myelin_BP.
PFam; PF01669; Myelin_MBP; 1.
PRINTS; PR00212; MYELINMBP.
ProDom; PD004542; Myelin_BP; 1.
PROSITE; PS00569; MYELIN_MBP; 1.
SEQUENCE 173 AA; 18731 MW; 66B4D016E66081AA CRC64;

Query Match 100.0%; Score 94; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENPVVHFFKNIIVTPRT 17
DB 85 ENPVVHFFKNIIVTPRT 101

Search completed: February 22, 2006, 21:37:14
Job time : 13.304 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:31:15 ; Search time 1.7323 Seconds
(without alignments)
944.229 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFKNIVTPRP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	94	100.0	128	1 MBRTS	myelin basic prote
2	94	100.0	167	2 A37246	myelin basic prote
3	94	100.0	169	1 MB80B	myelin basic prote
4	94	100.0	171	1 MB80B	myelin basic prote
5	94	100.0	171	1 MB80B	myelin basic prote
6	94	100.0	197	1 MB80B	myelin basic prote
7	94	100.0	328	1 MB80B	golli-myelin basic
8	87	92.6	174	2 S08535	myelin basic prote
9	60	63.8	128	2 A60215	myelin basic prote
10	53	56.4	155	2 B32999	myelin basic prote
11	45	47.9	308	2 G64440	hypothetical prote
12	44	46.8	329	2 A57246	beta-tectorin prec
13	44	46.8	639	2 T46577	arylsulfatase (EC
14	43	45.7	14	2 S12904	protein kinase (EC
15	43	45.7	85	2 C89965	conserved hypothet
16	43	45.7	134	2 T28704	hypothetical prote
17	43	45.7	395	2 H72222	conserved hypothet
18	43	45.7	672	2 A11183	transcription regu
19	43	45.7	1124	2 B84742	probable receptor
20	42	44.7	435	2 AB3076	glutamine synthetase
21	42	44.7	435	2 G98210	glutamine synthetase
22	42	44.7	435	2 JC1301	glutamate-ammonia
23	42	44.7	672	2 AG1541	Similar to transcr
24	42	44.7	891	2 T40137	hypothetical serin
25	41	43.6	48	2 D82534	hypothetical prote
26	41	43.6	332	2 E70384	biotin synthase (E
27	41	43.6	480	2 A12308	cytochrome D ubiqu
28	41	43.6	646	2 A11174	internalin, probab
29	41	43.6	690	2 E84945	glycine-tRNA ligas

ALIGNMENTS

RESULT 1

MBRTS

Myelin basic protein S - rat
N:Alternate names: small myelin basic protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Apr-1984 #sequence revision 08-Feb-1996 #Text_change 09-Jul-2004
C:Accession: B24351; A90275; A94243; A21062; A03142
R:Schaich, M.; Budzinski, R.M.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
A:Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of the
A:Reference number: A24351; MUID:87026249; PMID:2429678
A:Accession: B24351
A:Molecule type: mRNA
A:Residues: 1-128 <SCH>
A:Cross-references: UNIPROT:P02688; UNIPARC:UPI0000163B8F; EMBL:M25889; NID:g205321; PIR:
R:Dunkley, P.R.; Carnegie, P.R.
Biochem. J. 141, 243-255, 1974
A:Title: Amino acid sequence of the smaller basic protein from rat brain myelin.
A:Reference number: A90275; MUID:75127359; PMID:4141893
A:Accession: A90275
A:Molecule type: protein
A:Residues: 2-128 <DUN>
A:Cross-references: UNIPARC:UPI000002ADB4
A:Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in th
R:McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapira, R.
Science 179, 478-480, 1973
A:Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen
A:Reference number: A94243; MUID:73180720; PMID:4122324
A:Accession: A94243
A:Molecule type: protein
A:Residues: 46-86 <MCF>
A:Cross-references: UNIPARC:UPI00001740CC
A:Note: the sequence reported for this encephalitogenic peptide differs from that shown
R:Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
Cell 34, 799-806, 1983
A:Title: Characterization of cloned cDNA representing rat myelin basic protein: absence
A:Reference number: A21062; MUID:84026484; PMID:6194889
A:Accession: A21062
A:Molecule type: mRNA
A:Residues: 1-124, 'I', 126-128 <ROA>
A:Cross-references: UNIPARC:UPI000002E780
A:Experimental source: strain Sprague-Dawley
C:Superfamily: myelin basic protein
C:Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy
F:2-128/Product: myelin basic protein S #status experimental <WAT>
F:2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #stat
F:105/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 128;

Best Local Similarity 100.0%; Pred. No. 9.6e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

hypothetical prote
hypothetical prote
cytosine/guanine d
probable peptide m
probable ribonucle
hypothetical prote
ATM-like protein l
hypothetical prote
protein F41H10.2 (l
glutamate racemase
hypothetical prote
hypothetical prote
C4-dicarboxylate-b
conserved hypothet
conserved hypothet
o-succinylbenzoate

30 41 43.6 892 2 T27005
31 40 42.6 192 2 AD2530
32 40 42.6 428 2 D96934
33 40 42.6 431 2 T50177
34 40 42.6 983 2 H72510
35 40 42.6 1162 2 T51040
36 40 42.6 2089 2 C85426
37 40 42.6 3738 2 T05501
38 39 41.5 164 2 F88690
39 39 41.5 250 2 B81262
40 39 41.5 270 2 F86897
41 39 41.5 323 2 T15311
42 39 41.5 333 2 S18578
43 39 41.5 337 2 F89944
44 39 41.5 431 2 H70302
45 39 41.5 471 2 AB0308

Qy 1 ENPVVHFFKNIVTPRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 81 ENPVVHFFKNIVTPRTP 97

RESULT 2

A37246
myelin basic protein - guinea pig
N/Alternate names: myelin A1 protein
C/Species: Cavia porcellus (guinea pig)
C/Date: 31-Jul-1991 #sequence revision 31-Jul-1991 #text_change 09-Jul-2004
C/Accession: A37246; C92087; A03140
R/Deibler, G.E.; Martenson, R.B.; Krutzsch, H.C.; Kies, M.W.
J. Neurochem. 43, 100-105, 1984
A/Title: Sequence of guinea pig myelin basic protein.
A/Reference number: A37246; MUID:84215086; PMID:6202840
A/Accession: A37246
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-167 <DBI>
A/Cross-references: UNIPROT:P25188; UNIPARC:UPI000012BD39
R/Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
J. Biol. Chem. 246, 4630-4640, 1971
A/Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
A/Reference number: A92087
A/Accession: C92087
A/Molecule type: protein
A/Residues: 45-87 <SHA>
A/Cross-references: UNIPARC:UPI000017780D
C/Superfamily: myelin basic protein
C/Keywords: myelin

Query Match 100.0%; Score 94; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 3

MBB08
myelin basic protein - bovine
N/Alternate names: myelin A1 protein
N/Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
C/Species: Bos primigenius taurus (cattle)
C/Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 09-Jul-2004
C/Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
R/Eylar, E.H.; Brostoff, S.; Hasham, G.; Caccam, J.; Burnett, P.
J. Biol. Chem. 246, 5770-5784, 1971
A/Title: Basic A1 protein of the myelin membrane. The complete amino acid sequence.
A/Reference number: A92089; MUID:72007306; PMID:5096093
A/Accession: A92089
A/Molecule type: protein
A/Residues: 1,'S',2-169 <EYL>
A/Cross-references: UNIPROT:P02687; UNIPARC:UPI0000148533
R/Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
J. Biol. Chem. 249, 559-567, 1974
A/Title: Specific cleavage of the A1 protein from myelin with cathepsin D.
A/Reference number: A92160; MUID:74070688; PMID:4129204
A/Accession: A92160
A/Molecule type: protein
A/Residues: 1-169 <BRO>
A/Cross-references: UNIPARC:UPI000012BD38
R/Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
J. Biol. Chem. 246, 4630-4640, 1971
A/Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
A/Reference number: A92087
A/Accession: A92087
A/Molecule type: protein
A/Residues: 43-87 <SHA>

A/Cross-references: UNIPARC:UPI00001740BD
R/Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A/Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in gli
A/Reference number: S54343; MUID:95194333; PMID:7887910
A/Accession: S54343
A/Molecule type: protein
A/Residues: 74-75,'HG',78-82,'D',84-88,'105','X',107-108,'X',110-114,'X',116-119 <OKA>
A/Cross-references: UNIPARC:UPI00001740BE; UNIPARC:UPI00001740BF
R/Takamatsu, K.; Tatamoto, K.
Neurochem. Res. 17, 239-246, 1992
A/Title: Isolation and characterization of two novel peptide amides originating from my
A/Reference number: A61641; MUID:92319189; PMID:1377792
A/Accession: A61641
A/Molecule type: protein
A/Residues: 1-12 <TAK>
A/Cross-references: UNIPARC:UPI00001740C0
A/Accession: B61641
A/Molecule type: protein
A/Residues: 1-16 <TA2>
A/Cross-references: UNIPARC:UPI00001740C0
A/Note: these peptides have carboxyl-terminal amides probably produced by a non-enzymat
R/Brostoff, S.; Eylar, E.H.
Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
A/Title: Localization of methylated arginine in the A1 protein from myelin.
A/Reference number: A93777; MUID:71153946; PMID:4994464
A/Contents: annotation
A/Note: Arg-106 is modified to monomethylarginine and dimethylarginine
R/Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, F.C.; Robinson, A.B.
Science 168, 1220-1223, 1970
A/Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site of
A/Reference number: A94241; MUID:70178977; PMID:5442707
A/Contents: annotation
A/Note: the region including residues 114-122 induces experimental allergic encephalomy
C/Superfamily: myelin basic protein
C/Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune enceph
F/1-16/Product: myelin basic protein #status experimental <MAT>
F/1-16/Product: myelin peptide amide-16 #status experimental <PA16>
F/1-12/Product: myelin peptide amide-12 #status experimental <PA12>
F/1/Modified site: acetylated amino end (Ala) #status experimental
F/12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide am
F/16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide am
F/106/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
| | | | | | | | | | | | | | | | | | | | |
Db 82 ENPVVHFFKNIVTPRTP 98

RESULT 4
MBCZB
myelin basic protein - chimpanzee (tentative sequence)
N/Alternate names: MBP
C/Species: Pan troglodytes (chimpanzee)
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C/Accession: A03139
R/Westall, F.C.; Thompson, M.; Kalter, S.S.
Life Sci. 17, 219-223, 1975
A/Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
A/Reference number: A03139; MUID:76009821; PMID:51459
A/Accession: A03139
A/Molecule type: protein
A/Residues: 1-171 <WES>
A/Cross-references: UNIPROT:P06906; UNIPARC:UPI000012ED3D
C/Comment: This protein may function in maintaining the proper structure of myelin.
C/Superfamily: myelin basic protein
C/Keywords: blocked amino end; methylated amino acid; myelin; structural protein
F/1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F/107/Modified site: omega-N-methylarginine or omega-N,omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVMHFFKNIPTPTP 17
DB 83 ENPVMHFFKNIPTPTP 99

RESULT 5
MBPGS
myelin basic protein - pig (tentative sequence)
N;Alternate names: myelin A1 protein
N;Contains: myelin basic protein amide 14
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004
C;Accession: A61640; A36245
R;Kira, J.; Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.
J. Neurochem. 44, 134-142, 1985
A;Title: Amino acid sequence of porcine myelin basic protein.
A;Reference number: A61640; MUID:85056964; PMID:2578056
A;Accession: A61640
A;Molecule type: protein
A;Residues: 1-171 <KIR>
A;Cross-references: UNIPROT:P81558; UNIPARC:UPI000012ED3E
A;Note: some peptides were ordered by homology
R;Takamatsu, K.; Tatamoto, K.
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
A;Title: Isolation and characterization of a novel peptide amide from porcine brain.
A;Reference number: A36245; MUID:91058553; PMID:1700904
A;Accession: A36245
A;Molecule type: protein
A;Residues: 1-14 <TAK>
A;Cross-references: UNIPARC:UPI00001740C2
A;Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu
A;Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic
C;Superfamily: myelin basic protein
C;Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune encephal
F;1-171/Product: myelin basic protein #status experimental <MAT>
F;1-14/Product: myelin peptide amide-14 #status experimental <PA12>
F;1/Modified site: acetylated amino end (Ala) #status experimental
F;14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide ami
F;107/Modified site: omega-N-methylarginine or omega-N',omega-N'-dimethylarginine (Arg) (

Query Match 100.0%; Score 94; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVMHFFKNIPTPTP 17
DB 83 ENPVMHFFKNIPTPTP 99

RESULT 6
MBHUB
myelin basic protein [validated] - human
N;Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein prec
.5K splice form
C;Species: Homo sapiens (man)
C;Date: 18-Dec-1981 #sequence_revision 25-Aug-1995 #text_change 09-Jul-2004
C;Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219; I56
R;Streicher, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 370, 503-510, 1989
A;Title: The organization of the human myelin basic protein gene. Comparison with the mo
A;Reference number: S10482; MUID:89302693; PMID:2472816
A;Accession: S10482
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-197 <STR>
A;Cross-references: UNIPROT:P02686; UNIPARC:UPI000002ADA4; EMBL:X17286; EMBL:X17286; NID:934490; PIDN
R;Kamholz, J.; De Ferri, F.; Puckett, C.; Lazzarini, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-59 <RES>
A;Cross-references: UNIPARC:UPI000016AD10; GB:M63599; NID:G187402; PIDN:AAA59560.1; PID:
R;Roth, H.J.; Kronquist, K.E.; Kerlero de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 17, 321-328, 1987
A;Title: Evidence for the expression of four myelin basic protein variants in the develop
A;Reference number: I56567; MUID:87311781; PMID:2442403
A;Accession: I56567
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-132,144-197 <RE2>
A;Cross-references: UNIPARC:UPI000002ADAS5; GB:M30516; NID:G187410; PIDN:AAA59563.1; PID:
A;Accession: I73634
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-197 <RE3>
A;Cross-references: UNIPARC:UPI000002ADAA4; GB:M30515; NID:G187412; PIDN:AAA59564.1; PID:
R;Roth, H.J.; Kronquist, K.; Pretorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
J. Neurosci. Res. 16, 227-238, 1986
A;Title: Isolation and characterization of a cDNA coding for a novel human 17.3K myelin
A;Reference number: I56565; MUID:86308101; PMID:2427738
A;Accession: I56565
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-59,86-133,145-197 <RE4>
A;Cross-references: UNIPARC:UPI000002ADAA7; GB:M30047; NID:G187400; PIDN:AAA59559.1; PID:
R;Boullas, C.; Pang, H.; Mastrionardi, F.; Moscarello, M.A.
Arch. Biochem. Biophys. 322, 174-182, 1995
A;Title: The isolation and characterization of four myelin basic proteins from the unbo
A;Reference number: S66383; MUID:96004793; PMID:7574672
A;Accession: S66383
A;Molecule type: protein
A;Residues: 23-25,'X',27-39 <BOU>
A;Cross-references: UNIPARC:UPI00001740BC
C;Comment: Four alternatively spliced forms of myelin basic protein have been observed.
C;Genetics:
A;Gene: GDB:MBP
A;Cross-references: GDB:I19379; OMIM:159430
A;Map position: 18q22-18qter
A;Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
C;Function:
A;Description: probably helps maintain myelin structure
C;Superfamily: myelin basic protein
C;Keywords: acetylated amino end; alternative splicing; citrulline; experimental autoimm
F;2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MAT1>
F;2-132,144-197/Product: myelin basic protein, 20.2K splice form #status predicted <MAT2>
F;2-59,86-197/Product: myelin basic protein, 18.5K splice form #status experimental <MAT3>
F;2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
F;26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experiment
F;134/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg)

Query Match 100.0%; Score 94; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ENPVVHFPPKNIIVTRTP 17
|||||
Db 110 ENPVVHFPPKNIIVTRTP 126
|||||

RESULT 7
MBMSB
N;Alternate names: golli-mbp precursor - mouse
N;Contains: myelin basic protein
C;Species: Mus musculus (house mouse)
C;Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: A45421; A90875; A90867; A26591; A60920; I48407; I58996; I54
R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Amur-Umarjee, S.; Landry,
J. Biol. Chem. 268, 4930-4938, 1993
A;Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that e

A;Reference number: A45421; MUID:93186801; PMID:7680345
A;Accession: A45421
A;Molecule type: mRNA
A;Residues: 1-190;217-276;316-328 <CAM1>
A;Cross-references: UNIPROT:P04370; UNIPARC:UPI00001740C3; UNIPARC:UPI00001740C4; UNIPAR
A;Experimental source: clone J37
A;Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified
A;Accession: B45421
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-191,'SSEP' <CAM2>
A;Cross-references: UNIPARC:UPI0000004029; GB:L07508; NID:G193586; PIDN:AAA37721.1; PID
A;Experimental source: clone BG21
A;Note: sequence extracted from NCBI backbone (NCBIN:126700, NCBI:P:126715)
R;de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molineaux, S.; Lazzarin
Cell 43, 721-727, 1985
A;Title: Alternative splicing accounts for the four forms of myelin basic protein.
A;Reference number: A90875; MUID:86079555; PMID:2416470
A;Accession: A90875
A;Molecule type: mRNA
A;Residues: 134-328 <DEF>
A;Cross-references: UNIPARC:UPI000002ADAA9; GB:L00404; GB:M11669; NID:G199060; PIDN:AAA
A;Experimental source: 21.5K
R;Takahashi, N.; Roach, A.; Teplov, D.B.; Prusiner, S.B.; Hood, L.
Cell 42, 139-148, 1985
A;Title: Cloning and characterization of the myelin basic protein gene from mouse: one
A;Reference number: A90867; MUID:85254913; PMID:2410136
A;Accession: A90867
A;Molecule type: DNA
A;Residues: 134-190;217-328 <PAK>
A;Cross-references: UNIPARC:UPI00001740C6; UNIPARC:UPI00001740C7; GB:M11533; NID:G19904
A;Experimental source: 18.5K
R;Newman, S.; Kitamura, K.; Campagnoni, A.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
A;Title: Identification of a cDNA coding for a fifth form of myelin basic protein in mo
A;Reference number: A94188; MUID:87118269; PMID:2433693
A;Accession: A26591
A;Molecule type: mRNA
A;Residues: 134-274;316-328 <NEW1>
A;Cross-references: UNIPARC:UPI00001740C5; UNIPARC:UPI00001740C8; GB:M15060; NID:G19904
A;Experimental source: clone M722; splice form 17.22K
A;Accession: B26591
A;Molecule type: mRNA
A;Residues: 134-190;217-263;275-328 <NEW2>
A;Cross-references: UNIPARC:UPI00001740C6; UNIPARC:UPI00001740C9; UNIPARC:UPI00001740CA
A;Experimental source: clone M78; splice form 17.24K
R;Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V.W
J. Neurochem. 54, 2032-2041, 1990
A;Title: Expression of a novel transcript of the myelin basic protein gene.
A;Reference number: A60920; MUID:90250449; PMID:1692584
A;Accession: A60920
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 134-190;217-274;316-328 <KIT>
A;Cross-references: UNIPARC:UPI00001740C5; UNIPARC:UPI00001740C6; UNIPARC:UPI00001740CB
A;Experimental source: M41; splice form 14K
R;Grima, B.; Zelenika, D.; Pessac, B.
J. Neurochem. 59, 2318-2323, 1992
A;Title: A novel transcript overlapping the myelin basic protein gene.
A;Reference number: I48407; MUID:93057537; PMID:1279125
A;Accession: I48407
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-191,'SSEP' <GRI>
A;Cross-references: UNIPARC:UPI0000004029; EMBL:X67319; NID:G51332; PIDN:CAA47733.1; PI
A;Note: submitted to the EMBL Data Library, July 1992
R;Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
A;Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin ba
A;Reference number: I58996; MUID:84119431; PMID:6198644
A;Accession: I58996
A;Status: preliminary; translated from GB/EMBL/DBJ


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Query Match      47.9%; Score 45; DB 2; Length 308;
Best Local Similarity 70.0%; Pred. No. 6.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ENPVVHFFKN 10
    ||||: |||
Db 35 ENPVIQYFKN 44

RESULT 12
A57246
beta-tectorin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57246
R;Killick, R.; Legan, P.K.; Malenczak, C.; Richardson, G.P.
J. Cell Biol. 129, 535-547, 1995
A;Title: Molecular cloning of chick beta-tectorin, an extracellular matrix molecule of
A;Reference number: A57246; MUID:95238547; PMID:7721949
A;Accession: A57246
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-329 <KIL>
A;Cross-references: UNIPROT:P54097; UNIPARC:UPI0000136B89; GB:L38519; NID:g602439; PIDN:
C;Keywords: extracellular matrix; membrane protein; phosphatidylinositol linkage

Query Match      46.8%; Score 44; DB 2; Length 329;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIVT 13
    ||||| |||: |||
Db 91 KNPVTHFNISVS 103

RESULT 13
T46577
arylsulfatase (EC 3.1.6.1) [validated] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: T46577
R;Baker, D.L.; Paietta, J.V.
submitted to the EMBL Data Library, February 1997
A;Description: Molecular characterization of the arylsulfatase gene of Neurospora crassa
A;Reference number: 223090
A;Accession: T46577
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-639 <BAK>
A;Cross-references: UNIPROT:O43113; UNIPARC:UPI000006B2E2; EMBL:U89492; PIDN:AAC02716.1
A;Experimental source: strain wild type 74-OR23-1A
C;Genetics:
A;Gene: ars-1
A;Map position: 7
A;Introns: 115/1; 518/3
C;Function:
A;Description: EC 3.1.6.1 [validated, MUID:89384589]
A;Note: Genes are expressed under conditions of sulfur limitation and are under coordina
C;Superfamily: arylsulfatase, plant type
C;Keywords: sulfuric ester hydrolase

Query Match      46.8%; Score 44; DB 2; Length 639;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFFKNIVTPRTP 17
    |||: |||
Db 282 HLFDPDIVPRTTP 293

RESULT 14
S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
```

```
C;Species: Pisaster ochraceus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S12904
R;Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Burs, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A;Title: Identification of the sites in myelin basic protein that are phosphorylated by
A;Reference number: S12904; MUID:91032186; PMID:1699809
A;Accession: S12904
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <SAN>
A;Cross-references: UNIPROT:Q7M3M4; UNIPARC:UPI000017BF0C
C;Keywords: phosphotransferase

Query Match      45.7%; Score 43; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NIVTPRTP 17
    ||||| |||
Db 1 NIVTPRTP 8

RESULT 15
C89965
conserved hypothetical protein SA1613 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C89965
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hizamatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <KUR>
A;Cross-references: UNIPROT:Q99T75; UNIPARC:UPI000013B193; GB:BA000018; PID:g13701588;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1613
C;Superfamily: conserved hypothetical protein HI1000

Query Match      45.7%; Score 43; DB 2; Length 85;
Best Local Similarity 35.7%; Pred. No. 3.3;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 VVHFFKNIVTPRTP 17
    :|||: |||
Db 8 MHFYQRFISPLTP 21

Search completed: February 22, 2006, 21:38:18
Job time : 2.7323 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:11 ; Search time 11.1572 Seconds
(without alignments)
669.475 Million cell updates/sec

Title: US-10-000-439-13

Perfect score: 94
Sequence: 1 ENPVVHFKNIVTPRTP 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	17	3 AAY69395	Peptide d
2	94	100.0	17	5 AAO20308	Myelin ba
3	94	100.0	17	5 AAE26359	Peptide r
4	94	100.0	17	5 AAE23935	Peptide a
5	94	100.0	17	6 ABP97941	Amino aci
6	94	100.0	17	6 ABR50663	Glycopept
7	94	100.0	17	6 AAO19672	Human mye
8	94	100.0	17	7 ADE50773	Wild-type
9	94	100.0	17	7 ADW36476	HLA bindi
10	94	100.0	17	7 ADW35045	HLA bindi
11	94	100.0	17	7 ADW33812	HLA bindi
12	94	100.0	17	8 ADK67704	Human mye
13	94	100.0	17	8 ADL18291	Human mye
14	94	100.0	17	9 AEB77584	MBP pepti
15	94	100.0	17	9 AEB86495	Myelin ba
16	94	100.0	18	2 AAR44115	Human mye
17	94	100.0	18	2 AAR95357	Residues
18	94	100.0	18	2 AAW73600	Human mye
19	94	100.0	18	3 AAY66533	Myelin ba
20	94	100.0	19	2 AAR32295	Sequence
21	94	100.0	19	2 AAR44114	Human mye
22	94	100.0	19	2 AAR44123	Human mye
23	94	100.0	19	2 AAR85132	Human MBP
24	94	100.0	19	2 AAW05719	Residues

25	94	100.0	19	2 AAR95366	Residues
26	94	100.0	19	2 AAR95355	Residues
27	94	100.0	19	2 AAR95358	Residues
28	94	100.0	19	2 AAW34183	Bt-MBP (84
29	94	100.0	19	2 AAW34180	Residues
30	94	100.0	19	2 AAW18021	Human BPP
31	94	100.0	19	2 AAW44071	Human mye
32	94	100.0	19	2 AAW73607	Human mye
33	94	100.0	19	2 AAW73616	Human mye
34	94	100.0	19	3 AAY58992	Myelin ba
35	94	100.0	19	3 AAY85560	Human MBP
36	94	100.0	19	3 AAY85550	Human MBP
37	94	100.0	19	3 AAY66532	Myelin ba
38	94	100.0	19	3 AAY66543	Myelin ba
39	94	100.0	19	3 AAB12618	Human mye
40	94	100.0	19	3 AAB12613	Human mye
41	94	100.0	19	4 AAM99040	Vaccine r
42	94	100.0	19	4 AAB74440	Ovalbumin
43	94	100.0	19	4 AAG65171	Myelin ba
44	94	100.0	19	5 ABG31665	Myelin ba
45	94	100.0	19	7 ADW35009	HLA bindi

ALIGNMENTS

RESULT 1
AAY69395
ID AAY69395 standard; peptide; 17 AA.
XX
AC AAY69395;
XX
DT 19-JUN-2000 (first entry)
XX
DE Peptide derived from a human myelin basic protein.
XX
KW Human; myelin basic protein; oligodendroglial cell; Th2 immune response;
KW Th2-type cytokine; analogue; multiple sclerosis.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200011027-A1.
XX
PD 02-MAR-2000.
XX
PF 19-AUG-1999; 99WO-US019033.
XX
PR 20-AUG-1998; 98US-00137759.
XX
(NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
XX
PI Gaur A, Conlon P, Ling NC, Staehlin T, Crowe P;
XX WPI; 2000-224661/19.
XX
PT Inducing a Th2 immune response and a persistent systemic immune response
PT to myelin basic protein, MBP, or a peptide analog of MBP for use in
PT treating multiple sclerosis, by administering compositions comprising
XX peptide analogs of MBP.
XX
PS Example 10; Fig 8; 112pp; English.
XX
CC The present sequence represents a peptide derived from human myelin basic
CC protein. Myelin basic protein is found in the cytoplasm of human
CC oligodendroglial cells. Peptide analogue derived from the present
CC sequence is administered to a patient in need to induce a Th2 immune
CC response (i.e. production of T cells producing one or more Th2-type
CC cytokines) and/or a persistent systemic immune response to myelin basic
CC protein. These peptide analogues are at least seven amino acids long,
CC derived from residues 83-99 of human myelin basic protein and altered

CC from the native sequence at least at positions 91, 95 or 97. The peptide
 CC analogs are especially useful in the treatment of multiple sclerosis

SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTPRTP 17

RESULT 2
 AAO20308
 ID AAO20308 standard; peptide; 17 AA.

XX

AC AAO20308;

XX 31-MAY-2002 (first entry)

XX Myelin basic protein (MBP) epitope peptide region 83-99.

XX MBP; myelin basic protein; epitope; antiaesthetic; tolerogenic peptide;
 KW dermatological; antiallergic; neuroprotective; antithyroid; antinaemic;
 KW vasotropic; antiinflammatory; immunosuppressive; antidiabetic; class I;
 KW major histocompatibility complex; MHC; class II; autoimmune thyroiditis;
 KW hypersensitivity disorder; antigen; allergy; extrinsic asthma; utricaria;
 KW autoimmune haemolytic anaemia; atopic dermatitis; allergic rhinitis;
 KW autoimmune disease; multiple sclerosis; Grave's disease; sarcoidosis;
 KW systemic sclerosis; polymyositis; diabetes; transplant rejection;
 KW antiviral CD8+.

XX Unidentified.

XX WO2000216410-A2.

XX 28-FEB-2002.

XX 17-AUG-2001; 2001WO-GB003702.

XX 21-AUG-2000; 2000GB-00020618.

XX 14-JUN-2001; 2001GB-00014547.

XX (UYBR-) UNIV BRISTOL.

XX Wraith DC, Anderton SM, Mazza G, Ponsford M, Streeter HB;

XX WPT; 2002-292056/33.

XX Selecting tolerogenic peptide useful for treating autoimmune diseases
 PT e.g. multiple sclerosis, involves selecting peptide which binds major
 PT histocompatibility complex class I or II molecule without further
 PT processing.

XX Claim 12; Page 28; 55pp; English.

XX The invention relates to a method for selecting a tolerogenic peptide,
 CC comprising selecting a peptide which is capable of binding to a major
 CC histocompatibility complex (MHC) class I or II molecule without further
 CC processing. The peptides of the invention are useful for preventing a
 CC disease such as hypersensitivity disorder, and also for treating and/or
 CC preventing a disease in a subject. The method involves identifying an
 CC antigen for the disease, identifying an epitope (antigen processing
 CC independent epitope) for the antigen, and administering the epitope to
 CC the subject. The peptides of the invention are also useful for treating
 CC allergies such as extrinsic asthma, atopic dermatitis, allergic rhinitis,
 CC utricaria, autoimmune diseases such as multiple sclerosis, autoimmune
 CC thyroiditis, Grave's disease, systemic sclerosis, sarcoidosis, autoimmune
 CC haemolytic anaemia, polymyositis, diabetes, etc, and transplant
 CC rejection. The peptides are also useful for modifying antiviral CD8+
 CC responses in a tolerogenic fashion. This sequence represents an epitope

CC of the invention of peptide region 83-99 of Myelin basic protein (MBP)
 XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTPRTP 17

RESULT 3
 AAE26359
 ID AAE26359 standard; peptide; 17 AA.

XX

AC AAE26359;

XX 13-DEC-2002 (first entry)

XX Peptide related to myelin basic protein.

XX Th2 immune response; myelin basic protein; MBP; vaccine; MS;

XX Unidentified.

XX US6379670-B1.

XX 30-APR-2002.

XX 19-AUG-1999; 99US-00378244.

XX 18-NOV-1994; 94US-00342408.

XX 20-AUG-1998; 98US-00137759.

XX (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX (NOVS) NOVARTIS AG.

XX Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;

XX WPI; 2002-461895/49.

XX Inducing Th2 immune responses to Myelin Basic Protein (MBP) by
 PT administering the MBP peptide analog CGP 77116, useful for treating
 PT Multiple Sclerosis.

XX Disclosure; Col 35-36; 49pp; English.

XX The present invention relates to a novel method for inducing Th2 immune
 CC responses to Myelin Basic Protein (MBP) or a peptide analogue of MBP in a
 CC patient. The method involves administering a composition comprising the
 CC MBP peptide analogue CGP 77116 (NBI-5788). The method is useful for
 CC treating multiple sclerosis (MS). Sequences of the invention are also
 CC used as vaccines. The present sequence is a peptide related to human MBP

SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTPRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTPRTP 17

RESULT 4
 AAE23935
 ID AAE23935 standard; peptide; 17 AA.

XX

AC AAE23935;

XX 10-SEP-2002 (first entry)
 XX Peptide analogue used in the invention.
 XX Autoimmune disease; multiple sclerosis; MS; Jbeta; Cbeta; Vbeta; Dbeta;
 KW immunosuppressive; T-cell receptor; therapy.
 XX Unidentified.
 OS WO200216434-A1.
 XX PN 28-FEB-2002.
 XX PF 22-AUG-2000; 2000WO-US022988.
 XX PR 22-AUG-2000; 2000WO-US022988.
 XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Zhang JZ;
 XX WPI; 2002-454317/48.
 XX A novel peptide used in the treatment of autoimmune disease e.g. multiple
 PT sclerosis.
 XX Example 2; Fig 2; 64pp; English.
 PS The invention relates to a peptide used in the treatment of autoimmune
 CC disease e.g. multiple sclerosis (MS). More particularly, it concerns a T-
 CC cell receptor sequence found in some MS patients and methods for its
 CC detection. T cell receptors comprise alpha and beta chains, with beta
 CC chains comprising the following regions from N-terminus to C-terminus:
 CC Vbeta-Dbeta-Jbeta-Cbeta. T cell receptors naturally vary in the Vbeta-
 CC Dbeta-Jbeta region. The peptides of the invention are used for treating
 CC autoimmune disease e.g. multiple sclerosis. The present sequence is a
 CC peptide analogue used in the exemplification of the invention
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 94; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIPTPT 17
 DB 1 ENPVVHFFKNIPTPT 17
 RESULT 5
 ID ABP97941 standard; peptide; 17 AA.
 XX AC ABP97941;
 XX 17-JUN-2003 (first entry)
 XX Amino acid sequence of a glycopeptide.
 XX Glycopeptide; serum; immunoabsorption column; antibody;
 KW multiple sclerosis.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "H attached"
 FT Modified-site 2 /note= "glycosylated residue"
 FT Modified-site 17 /note= "OH attached"
 XX

PN WO2003009887-A2.
 XX 06-FEB-2003.
 XX 25-JUL-2002; 2002WO-EP008274.
 XX 25-JUL-2001; 2001IT-FI000144.
 XX (UYFI-) UNIV FIRENZE.
 XX Pinto F, Papini AM, Chelli M, Rovero P, Lolli F;
 XX WPI; 2003-312632/30.
 XX Immunoabsorption column, useful for treating multiple sclerosis, contains
 PT glycopeptides able to react with disease-specific autoantibodies.
 XX Claim 4; Page 6; 13pp; English.
 XX ABP97937-44 represent glycopeptides of a formula given in the
 CC specification. The glycopeptides are used to produce columns of the
 CC invention. The specification describes immunoabsorption columns,
 CC containing conjugates comprising glycopeptides which are able to
 CC recognize antibodies implicated in multiple sclerosis. The column removes
 CC harmful antibodies selectively, leaving all other components of the serum
 CC unchanged. The column is used to treat multiple sclerosis
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 94; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIPTPT 17
 DB 1 ENPVVHFFKNIPTPT 17
 RESULT 6
 ID ABR56063 standard; peptide; 17 AA.
 XX AC ABR56063;
 XX 06-AUG-2003 (first entry)
 XX Glycopeptide #5 for diagnosis and treatment of multiple sclerosis.
 XX Glycopeptide; neuroprotective; autoantibody; multiple sclerosis.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 2 /note= "Asn(Glc)"
 XX WO2003000733-A2.
 XX 03-JAN-2003.
 XX 19-JUN-2002; 2002WO-EP006767.
 XX 22-JUN-2001; 2001IT-FI000114.
 XX (UYFI-) UNIV FIRENZE.
 XX Papini AM, Chelli M, Rovero P, Lolli F;
 XX WPI; 2003-354383/33.
 XX Novel glycopeptides comprising a specific tetrapeptide, useful as
 PT diagnostic tools for identifying multiple sclerosis.
 XX

PS Claim 7; Page 12; 14pp; English.

XX The present invention relates to glycopeptides (ABR56059-ABR56066). The glycopeptides have high specificity in recognizing autoantibodies involved in multiple sclerosis pathology, and thus are effectively used in diagnosis and treatment for multiple sclerosis

XX Sequence 17 AA;

Query Match 100.0%; Score 94; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
Db 1 ENPVVHFFKNIIVTRTP 17

RESULT 7

AA019672
ID AA019672 standard; peptide; 17 AA.

XX AA019672;

XX 28-MAR-2003 (first entry)

XX Human myelin basic protein MBP minimal epitope.

XX Human; Ig; immunoglobulin; immunotherapy; immune disease; MBP; Fcpsiilon receptor; autoimmune disease; constant region; heavy chain; antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2; antiarthritic; antirheumatic; antidiabetic; neuroprotective; myelin basic protein; minimal epitope.

XX Homo sapiens.

XX WO200298317-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013527.

XX 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

XX (REGC) UNIV CALIFORNIA.

XX Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

XX New fusion molecules comprising polypeptide sequences that bind to IgG inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

XX Claim 23; Page 116; 116pp; English.

XX The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcpsiilonR). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-I diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present sequence is the human myelin

CC basic protein minimal epitope which can be used in a fusion protein of the invention

XX Sequence 17 AA;

Query Match 100.0%; Score 94; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENPVVHFFKNIIVTRTP 17
Db 1 ENPVVHFFKNIIVTRTP 17

RESULT 8

ADE50773
ID ADE50773 standard; peptide; 17 AA.

XX ADE50773;

XX 29-JAN-2004 (first entry)

XX Wild-type human myelin basic protein peptide analog.

XX Human; Th2; immune response; myelin basic protein; peptide analog; proteolysis; multiple sclerosis; neuroprotective; gene therapy.

XX Homo sapiens.

XX US2002176866-A1.

XX 28-NOV-2002.

XX 20-MAR-2002; 2002US-00104973.

XX 18-NOV-1994; 94US-00342408.

XX 20-AUG-1998; 98US-00137759.

XX 19-AUG-1999; 99US-00378244.

XX (NEUR-) NEUROCRINE BIOSCIENCES INC.

XX Gaur A, Conlon P, Ling NC, Staehelin T, Crowe PD;

XX WPI; 2003-615722/58.

XX Inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, useful for treating multiple sclerosis, comprises administering an amount of a pharmaceutical composition comprising a peptide analog.

XX Disclosure; SEQ ID NO 3; 52pp; English.

XX The invention discloses a method for inducing a Th2 immune response to myelin basic protein or its peptide analog in a patient, comprising administering a composition comprising a peptide analog in combination with a carrier/adjvant or diluent. The peptide analog comprises at least 7 amino acids selected from residues 83 to 99 of human myelin basic protein, where: the L-lysine at position 91, L-arginine at position 97 or L-threonine at position 95, is altered to another amino acid, and one to three L-amino acids selected from valine at position 86 or 87, histidine at position 88, threonine at position 95 or 98, and proline at position 99 are altered to an amino acid other than the amino acid present in the native protein at that position or the L-lysine at position 91 is altered to another amino acid and the N- and/or C-terminal amino acid are altered to another amino acid, such that upon administration of the peptide analog in vivo proteolysis is reduced. The peptide analog comprises 7-17 amino acids and one to four additional altered residues. The N-terminal amino acid is residue 83 of human myelin basic protein. At least one of the additional L-amino acids selected from residues 83 to 90 and 92 to 99 is substituted with a charged amino acid. The method is useful for treating multiple sclerosis using peptide analogs of human myelin basic protein. The sequence presented is the wild-type human myelin basic protein peptide analog.

Qy	1	ENPVVHFFKNIVTPRTP	17	
Db	1	ENPVVHFFKNIVTPRTP	17	
RESULT 10				
ADW35045	ADW35045 standard; peptide; 17 AA.			
XX	AC	AC		
XX	ADW35045;			
XX	10-MAR-2005	(first entry)		
DT				
XX	HLA binding epitope #5795.			
DE				
XX				
KW	Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;			
KW	MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;			
KW	viral disease; cancer.			
XX				
OS	Unidentified.			
XX				
PN	WO2003040165-A2.			
XX				
PD	15-MAY-2003.			
XX				
PF	18-OCT-2001; 2001WO-US051650.			
XX				
PR	19-OCT-2000; 2000US-0242350P.			
PR	20-APR-2001; 2001US-0285624P.			
XX				
PA	(EPIM-) EPIMMUNE INC.			
XX				
PI	Sette A, Sidney J, Southwood S;			
XX				
DR	WPI; 2003-441519/41.			
XX				
PT	New composition comprising at least one peptide having allele-specific			
PT	binding motifs for HLA, useful for preventing, treating or diagnosing			
PT	viral diseases and cancer.			
XX				
PS	Claim 1; Page 52-379; 382pp; English.			
XX				
CC	The invention relates to a composition comprising at least one peptide			
CC	having an isolated, prepared epitope selected from any of the sequences			
CC	from 30 lists given in the specification. Also disclosed is a method for			
CC	inducing a cytotoxic T cell response against a pre-selected antigen in a			
CC	patient expressing a specific MHC class I allele by contacting cytotoxic			
CC	T cells from the patient with the composition cited above. The			
CC	composition comprises an epitope that is joined by an amino acid linker.			
CC	The epitope is admixed or joined to a CTL or HTL epitope. Where when an A2			
CC	bound to an HLA molecule on the antigen-presenting cell, where when an A2			
CC	-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL			
CC	binds to a complex of the HLA molecule and the epitope. Specifically			
CC	claimed are peptides having allele-specific binding motifs for HLA. The			
CC	compositions and methods are useful for preventing, treating or			
CC	diagnosing viral diseases and cancer. The peptide epitopes are useful as			
CC	diagnostic agents for evaluating immune responses, for making antibodies			
CC	and for evaluating efficacy of a vaccine. Sequences given in ADW29251-			
CC	ADW37745 represent epitopes of the invention as given in Tables 2-31.			
XX				
XX				
SQ	Sequence 17 AA;			
Query Match 100.0%; Score 94; DB 7; Length 17;				
Best Local Similarity 100.0%; Pred No. 7e-09;				
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	ENPVVHFFKNIVTPRTP	17	
Db	1	ENPVVHFFKNIVTPRTP	17	
RESULT 11				
ADW33812	ADW33812			

ID ADW33812 standard; peptide; 17 AA.
 AC ADW33812;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #4562.
 XX
 KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.
 XX
 OS Unidentified.
 XX
 FN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PP 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI; 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 DB 1 ENPVVHFFKNIVTPRTP 17
 RESULT 12
 ADK67704
 ID ADK67704 standard; peptide; 17 AA.
 AC ADK67704;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human myelin basic protein peptide fragment MBP-1 (aa110-126).

XX
 KW Human; myelin basic protein; vaccine; multiple sclerosis; T cell.
 XX
 OS Homo sapiens.
 XX
 PN WO2004015070-A2.
 XX
 PD 19-FEB-2004.
 XX
 XX 06-AUG-2003; 2003WO-US024548.
 PF
 XX 08-AUG-2002; 2002US-0402521P.
 XX
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (OPEX-) OPEXA PHARM INC.
 XX
 PI Zhang JZ;
 XX
 XX WPI; 2004-180654/17.
 DR
 XX Isolating one or more T cells specific for an antigen of interest
 PT comprises incubating a T cell sample with an antigen, useful for
 PT diagnosing or treating multiple sclerosis, psoriasis, thyroiditis,
 PT diabetes and rheumatoid arthritis.
 XX
 PS Example 1; SEQ ID NO 1; 38pp; English.
 XX
 CC The present invention is direct to methods of isolating antigen specific
 CC T cells, especially T cells specific for self or autoantigens. This
 CC comprises incubating a sample of T cells obtained from a patient with the
 CC antigen and selecting T cells that express one or more of first markers
 CC selected from CD69, CD4, CD25, CD36 and HLA-DR, and one or more second
 CC markers selected from interleukin-2, interferon-gamma, tumour necrosis
 CC factor alpha, interleukin-5, interleukin-10 and interleukin-12. The
 CC methods are useful for isolating autoreactive T cells which play a role
 CC in the pathogenesis of autoimmune diseases. The methods also permit the
 CC diagnosis of autoimmune disease as well as monitoring the progression of
 CC the disease and for monitoring the efficacy of treatment. The methods
 CC allow the preparation of autologous T cell vaccines for the treatment of
 CC T cell related autoimmune diseases. Vaccine preparation involves the
 CC isolation of antigen-specific T cells optionally followed by culturing
 CC steps which allow the expansion of the population of isolated antigen-
 CC specific T cells. An example from the invention describes the isolation
 CC of myelin-reactive T cells for T cell vaccination. Peripheral blood
 CC mononuclear cells were isolated from the blood of multiple sclerosis
 CC patients and incubated with peptides comprising known immunodominant
 CC regions of 3 myelin proteins. These included the present peptide, which
 CC comprises amino acids 110-126 of human myelin basic protein. Cells were
 CC then selected for the expression of gene products indicative of activated
 CC T cells, and myelin-reactive T cells were propagated in culture. The
 CC methods and compositions of the invention are useful for the diagnosis
 CC and/or treatment of autoimmune diseases or T cell associated conditions
 CC such as multiple sclerosis, myasthenia gravis, psoriasis, systemic lupus
 CC erythematosus, autoimmune thyroiditis, Grave's disease, inflammatory
 CC bowel disease, diabetes and rheumatoid arthritis.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 94; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIVTPRTP 17
 DB 1 ENPVVHFFKNIVTPRTP 17
 RESULT 13
 ADL18291
 ID ADL18291 standard; peptide; 17 AA.
 XX
 AC ADL18291;
 XX

DT 20-MAY-2004 (first entry)
 DE Human myelin basic protein (MBP), peptide #2.
 XX
 KW Demyelinating disease; neuron-specific antigen; human;
 KW myelin basic protein; MBP; myelin oligodendrocyte glycoprotein;
 KW myelin associated glycoprotein; MAG; proteolipid protein; PLP;
 KW small heat shock protein; transaldolase; Glial fibrillary protein;
 KW S-100 protein; cross-reactive peptide; glutamate receptor;
 KW phosphodiesterase; multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN US2004043431-A1.
 PD 04-MAR-2004.
 XX
 XX 29-AUG-2002; 2002US-00233892.
 XX
 XX 29-AUG-2002; 2002US-00233892.
 XX
 XX (VOJD/) VOJDANI A.
 XX
 XX Vojdani A;
 XX
 XX WPI; 2004-313756/29.
 XX
 XX Diagnosing likelihood and severity of demyelinating disease, by
 PT determining antibodies against neuron-specific antigen, comparing level
 PT of detected antibodies with normal level for detecting absence/likelihood
 PT of demyelinating disease.
 XX
 XX Claim 6; SEQ ID NO 2; 27pp; English.
 XX
 XX The present invention relates to a method of diagnosing the likelihood
 CC and severity of demyelinating diseases. The method involves determining
 CC antibodies against neuron-specific antigen in sample, comparing the level
 CC of antibodies with the normal level of antibodies, where normal level of
 CC antibodies for neuron-specific antigen indicate optimal conditions, lower
 CC than or higher than normal level of antibodies for the antigen indicate
 CC an absence of or a likelihood of demyelinating diseases, respectively.
 CC The neuron-specific antigen is chosen from myelin basic protein (MBP),
 CC myelin oligodendrocyte glycoprotein, myelin associated glycoprotein
 CC (MAG), proteolipid protein (PLP), small heat shock protein,
 CC transaldolase, Glial fibrillary protein, S-100 protein, cross-reactive
 CC peptide from dietary protein, cross-reactive peptide from infectious
 CC agent, glutamate receptor, and phosphodiesterase. The immunoassay is an
 CC enzyme linked immunosorbent assay (ELISA) test. The method is useful for
 CC diagnosing the likelihood and severity of demyelinating diseases such as
 CC multiple sclerosis in a patient. The present sequence represents a
 CC peptide from human MBP.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 94; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIIVTRTP 17
 DB 1 ENPVVHFFKNIIVTRTP 17
 RESULT 14
 AEB77584
 ID AEB77584 standard; peptide; 17 AA.
 XX
 AC AEB77584;
 XX
 XX 06-OCT-2005 (first entry)
 DT
 DE MBP peptide - SEQ ID 6.
 XX

KW autism; nootropic; asperger syndrome; MBP.
 XX
 OS Unidentified.
 XX
 PN US2005170333-A1.
 PD 04-AUG-2005.
 XX
 XX 03-FEB-2004; 2004US-00770712.
 XX
 XX 03-FEB-2004; 2004US-00770712.
 XX
 XX (VOJD/) VOJDANI A.
 XX
 XX Vojdani A;
 XX
 XX WPI; 2005-562713/57.
 XX
 XX Determining etiology of autistic spectrum disorder in patient, by
 PT determining level of infectious agent/toxic chemical/dietary protein
 PT derived antigen in samples of patient, comparing it with normal level of
 PT antigens of control subjects.
 XX
 XX Disclosure; SEQ ID NO 6; 89pp; English.
 XX
 XX The invention comprises a method of determining etiology of an autistic
 CC spectrum disorder in a patient. The method involves determining the level
 CC of an infectious agent, toxic chemical, or dietary protein derived
 CC antigen, or their antibodies in samples of patient, and comparing
 CC antigens/antibodies levels with normal levels of antigens/antibodies from
 CC control subjects. The method of the invention is useful for determining
 CC the etiology of an autistic spectrum disorder, such as autism, pervasive
 CC development disorder and Asperger's syndrome. The present amino acid
 CC sequence represents a peptide that was used in the exemplification of the
 CC invention.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 94; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENPVVHFFKNIIVTRTP 17
 DB 1 ENPVVHFFKNIIVTRTP 17
 RESULT 15
 AEB86495
 ID AEB86495 standard; peptide; 17 AA.
 XX
 AC AEB86495;
 XX
 XX 20-OCT-2005 (first entry)
 DT
 DE Myelin basic protein (MBP) peptide, amino acids 83-99.
 XX
 KW pharmaceutical; t-lymphocyte; antigen; multiple sclerosis;
 KW autoimmune disease; immune disorder; immune stimulation; immunity;
 KW autoimmunity; immunosuppressive; neuroprotective; antiarthritic;
 KW antirheumatic; antiinflammatory; myelin; myelin basic protein; MBP.
 XX
 OS Unidentified.
 XX
 XX WO2005074579-A2.
 XX
 XX 18-AUG-2005.
 XX
 XX 02-FEB-2005; 2005WO-US002962.
 XX
 XX 02-FEB-2004; 2004US-0541397P.
 XX
 XX (MIXT-) MIXTURE SCI INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 FI Houghten RA, Pinilla C, Martin R, Sturzebecher C;
 PI Shukaliak-Quandt J, McFarland HF;
 XX
 DR WPI; 2005-555771/56.
 XX
 FT Complex peptide mixture having immunomodulatory effects, useful for
 PT preparing medicament for treating autoimmune disease e.g. multiple
 PT sclerosis, rheumatoid arthritis, for preparing medicament for stimulating
 XX immune cell.
 PS
 XX Example; Page 22; 51pp; English.
 CC
 CC The invention relates to complex peptide mixtures comprises several
 CC peptides having 8-20 amino acids, where the mixture comprises peptides
 CC having a degree of diversity at defined positions in the peptide chain,
 CC where the degree of diversity in the defined position is different from
 CC other defined positions, and where in the majority of the mixture, the
 CC peptides includes Ala, Glu, Lys and Tyr and no other amino acids, in at
 CC least four positions. Also described are: (1) a method of creating a high
 CC affinity peptide ligand of a defined formula for a receptor of a T cell
 CC that is reactive to a myelin antigen, copolymer, or an active mixture;
 CC and (2) a method of enhancing a biological property of a complex mixture
 CC of peptides, peptidomimetics or peptides and peptidomimetics. The
 CC complex peptide mixture is useful in the preparation of a medicament for
 CC treating a disease such as multiple sclerosis (MS) and experimental
 CC autoimmune encephalomyelitis (EAE). It is also useful for preparing a
 CC medicament for stimulating an immune cell, or for suppression of an
 CC immune reaction (e.g. autoimmune reaction) to an antigen derived from
 CC myelin. This sequence represents a myelin peptide used in the examples of
 CC the present invention.
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 94; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7e-09;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENPVVHFFKNIVTRTP 17
 |||||
 Db 1 ENPVVHFFKNIVTRTP 17

Search completed: February 22, 2006, 21:30:49
 Job time : 14.1572 secs

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:24 ; Search time 154.266 Seconds
(without alignments)
1061.041 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTTPCPPAPELL.....MHEALHHYQRRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 IGHG1_HUMAN	P01857 homo sapien
2	1225	97.2	465	2 Q6GNX6_HUMAN	Q6gnx6 homo sapien
3	1225	97.2	466	2 Q6IN78_HUMAN	Q6in78 homo sapien
4	1225	97.2	469	2 Q569F4_HUMAN	Q569f4 homo sapien
5	1225	97.2	469	2 Q7Z7P5_HUMAN	Q7z7p5 homo sapien
6	1225	97.2	470	2 Q7Z5W1_HUMAN	Q7z5w1 homo sapien
7	1225	97.2	470	2 Q6PJA4_HUMAN	Q6pja4 homo sapien
8	1225	97.2	472	2 Q6N089_HUMAN	Q6n089 homo sapien
9	1225	97.2	475	2 Q5EFE5_HUMAN	Q5efe5 homo sapien
10	1225	97.2	475	2 Q6GNW7_HUMAN	Q6gnw7 homo sapien
11	1225	97.2	476	2 Q6GNX1_HUMAN	Q6gnx1 homo sapien
12	1225	97.2	679	2 Q96PQ8_HUMAN	Q96pq8 homo sapien
13	1221	96.9	473	2 Q6P055_HUMAN	Q6p055 homo sapien
14	1221	96.9	475	2 Q6MZQ6_HUMAN	Q6mzq6 homo sapien
15	1221	96.9	480	2 Q6N094_HUMAN	Q6n094 homo sapien
16	1221	96.9	481	2 Q6N097_HUMAN	Q6n097 homo sapien
17	1221	96.9	482	2 Q7Z351_HUMAN	Q7z351 homo sapien
18	1219	96.7	348	2 Q6PYX1_HUMAN	Q6pyx1 homo sapien
19	1219	96.7	473	2 Q6MZV7_HUMAN	Q6mzv7 homo sapien
20	1219	96.7	478	2 Q6P181_HUMAN	Q6p181 homo sapien
21	1219	96.7	480	2 Q6PJF1_HUMAN	Q6pjf1 homo sapien
22	1218	96.7	466	2 Q6N096_HUMAN	Q6n096 homo sapien
23	1214	96.3	475	2 Q6N095_HUMAN	Q6n095 homo sapien
24	1214	96.3	544	2 Q6PJ95_HUMAN	Q6pj95 homo sapien
25	1196	94.9	487	2 Q6SZL2_HUMAN	Q6szl2 homo sapien
26	1164	92.4	475	2 Q5RE17_HUMAN	Q5re17 pongo pygma
27	1138	90.3	354	2 Q86TT2_HUMAN	Q86tt2 homo sapien
28	1138	90.3	518	2 Q6N030_HUMAN	Q6n030 homo sapien
29	1138	90.3	519	2 Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1134	90.0	521	2 Q8N4Y9_HUMAN	Q8ny9 homo sapien
31	1128	89.5	290	1 IGHG3_HUMAN	P01860 homo sapien

RESULT 1	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
ID	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	PROTEIN SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal			
RT	IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic			
RT	peptides of the H-chain, alignment of the tryptic peptides and			
RT	discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			

Q8NF17 homo sapien
P01859 homo sapien
Q6N093 homo sapien
Q6MZU6 homo sapien
Q6P6C4 homo sapien
P01861 homo sapien
Q8TC63 homo sapien
Q68CN4 homo sapien
Q6MX7 homo sapien
P01870 oryctolagus
Q95M34 equus cabal
P01862 cavia porce
P20761 rattus norv
Q5M839 rattus norv

RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
CC GIM(3) markers, 239-D and 241-L. KOL and EU sequences have the
CC GIM(3) marker and the GIM (non-1) markers.
CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT; Genomic_DNA.
DR PIR; A93433; GHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1AOK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DS1; X-ray; H=1-101.
DR PDB; 1DV6; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=106-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1H2H; X-ray; H/K=1-330.
DR PDB; 1I17; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1LOQ; X-ray; A/B=119-330.
DR PDB; 1T83; X-ray; A/B=107-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHL1.
DR MIM; 147100; .
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain.
FT REGION 1 98
CH1.

FT REGION 99 110
FT REGION 111 223
FT REGION 224 330
FT CARBOHYD 180 180
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT VARIANT 97 97
FT 239
FT VARIANT 241
FT 241
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FT STRAND 23 24
FT STRAND 26 33
FT STRAND 38 38
FT STRAND 41 41
FT TURN 42 45
FT TURN 48 49
FT STRAND 50 52
FT STRAND 57 58
FT TURN 59 61
FT STRAND 62 71
FT HELIX 73 75
FT TURN 76 78
FT STRAND 82 87
FT TURN 88 91
FT STRAND 92 97
FT TURN 102 103
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 149
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 167
FT STRAND 171 172
FT STRAND 176 177
FT TURN 179 180
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
FT STRAND 261 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 311
FT TURN 313 314
FT HELIX 316 318
FT STRAND 319 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 97.2%; Score 1225; DB 1; Length 330;
Best Local Similarity 97.0%; Pred. No. 5.9e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
Db 159 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQPENNYKTTTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 279 PVLDSGDSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
Q6GMX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR071110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
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Query Match 97.2%; Score 1225; DB 2; Length 465;
Best Local Similarity 97.0%; Pred. No. 9,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 234 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293
Qy 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
Db 294 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 353
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQPENNYKTTTP 180
Db 354 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAWESNGQPENNYKTTTP 413

RESULT 3
Q6IN78 HUMAN
ID Q6IN78 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR071110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
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DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCDE81076E CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 466;
 Best Local Similarity 97.0%; Pred. No. 9.1e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 235 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 294
 QY 61 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
 DB 295 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 354
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
 DB 355 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 414
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 415 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 466

RESULT 4
 Q569P4_HUMAN
 ID Q569P4_HUMAN PRELIMINARY; PRT; 469 AA.
 AC Q569P4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092518; AAH92518.1; -; mRNA.
 SQ SEQUENCE 469 AA; 51254 MW; AC134483047784F CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 469;
 Best Local Similarity 97.0%; Pred. No. 9.2e-90;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 238 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297
 QY 61 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
 DB 298 NWTVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 357
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
 DB 358 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 417
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
 DB 418 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 469

RESULT 5
 Q7Z7P5_HUMAN
 ID Q7Z7P5_HUMAN PRELIMINARY; PRT; 469 AA.
 AC Q7Z7P5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RG NIH MGC Project;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051328; AAH51328.1; -; mRNA.
 DR HSSP; P01857; 1HZH.
 DR SMR; Q7Z7P5; 20-469.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8DSBE12BAAF795C CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 469;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 238 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 297

QY 61 NNYVDGVEVHNKTKPRBEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 120
DB 298 NNYVDGVEVHNKTKPRBEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 357

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 358 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 417

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 418 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 469

RESULT 6
Q725W1_HUMAN
ID Q725W1_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -, mRNA.
DR HSP; P01857; IHZM.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298

QY 61 NNYVDGVEVHNKTKPRBEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 120
DB 299 NNYVDGVEVHNKTKPRBEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 358

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 359 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 419 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 7
Q6PJA4_HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RL NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSP; P01861; IADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 470;
Best Local Similarity 97.0%; Pred. No. 9.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 239 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 298
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 358
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 359 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCSVMEALHNHYQOORSLSLSPGK 232
DB 419 PVLDSGSPFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQOORSLSLSPGK 470

RESULT 8
Q6N089 HUMAN
ID Q6N089_HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
RT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -; mRNA.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 421 PVLDSGSPFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQOORSLSLSPGK 472

RESULT 9
Q5EFES HUMAN
ID Q5EFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q5EFES;
RT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC "Sequence determination of the recombinant human anti-Rhd monoclonal antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy chain.
FT SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 303
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
DB 304 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 363
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180

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Db 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDIWVESNGQPENNYKTPP 423
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYQOQSLSLSPGK 232
Db 424 PVLDSGDSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYQOQSLSLSPGK 475

RESULT 10
Q6GMW7 HUMAN
ID Q6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782.1; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1PE55D736860F8 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 475;
Best Local Similarity 97.0%; Pred. No. 9,3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCTCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 244 EPKSCDKHTCTCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 303
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QY 61 NWYDGVGVHNVKTKPREQYNSTYRVVSVLTVLHQNWNGKQYCKVKSNKALPAPIEKT 120
Db 304 NWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDMLNGKQYCKVKSNKALPAPIEKT 363
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDIWVESNGQPENNYKTPP 180
Db 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSPDIWVESNGQPENNYKTPP 423
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYQOQSLSLSPGK 232
Db 424 PVLDSGDSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYQOQSLSLSPGK 475

RESULT 11
Q6GMX1 HUMAN
ID Q6GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773.1; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
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Query Match

97.2%; Score 1225; DB 2; Length 476;

Best Local Similarity 97.0%; Pred. No. 9.3e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKF 60
DB 245 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKF 304

QY 61 NWYDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120
DB 305 NWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 364

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 365 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 424

QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCVMHEALHNHYQOQSLSLSPGK 232
DB 425 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCVMHEALHNHYQOQSLSLSPGK 476

RESULT 12
Q96PQ8_HUMAN
ID Q96PQ8_HUMAN PRELIMINARY; PRT; 679 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21477448; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK58686.2; -, mRNA.
DR HSP; P08709; IKLI.
DR SMR; Q96PQ8; 39-180, 191-444, 447-679.
DR Ensembl; ENSG00000057593; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_H.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLDOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS00026; EGF 3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00835; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 679 AA; 7552 MW; 0B0023AE70A067A1 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 679;
Best Local Similarity 97.0%; Pred. No. 1.5e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKF 60
DB 448 EPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDDEVKF 507

QY 61 NWYDGVGVHNVKTKPREEQYNSTYRVVSVLTVLHQNMNMGKEYCKVSNKALPAPIEKT 120
DB 508 NWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 567

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 568 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 627

QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCVMHEALHNHYQOQSLSLSPGK 232
DB 628 PVLDSVGSFPLYSKLTVDKSRWQGNVFSCVMHEALHNHYQOQSLSLSPGK 679

RESULT 13
Q6P055_HUMAN
ID Q6P055_HUMAN PRELIMINARY; PRT; 473 AA.
AC Q6P055;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.O.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

```
RT and mouse cDNA sequences. ";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC065920; AAH65920.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; IPR003599; Ig.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 473;
Best Local Similarity 96.6%; Pred. No. 1.9e-89;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 242 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 301

QY 61 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
DB 302 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 361

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 362 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 421

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
DB 422 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLHNNHYTKQSLSLSPGK 473

RESULT 14
Q6MZQ6 HUMAN
ID Q6MZQ6 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; IPR003599; Ig.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 480;
Best Local Similarity 96.6%; Pred. No. 2e-89;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303

QY 61 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNGKEYKCKVSNKALPAPIEKT 120
DB 304 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 363

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
DB 364 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 423

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
DB 424 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEGLHNNHYTKQSLSLSPGK 475

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ID Q6N094 HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O01196.
GN Name=DKFZp686O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; IPR003599; Ig.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match          96.9%; Score 1221; DB 2; Length 480;
Best Local Similarity 96.6%; Pred. No. 2e-89;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 244 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 303
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Db	249	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLWISRTPEVTCVWVDVSHEDPEVKF	308
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Db	309	NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKT	368
Qy	121	ISKAKVQPREPOVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP	180
Db	369	ISKAKGQPREPQVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP	428
Qy	181	PVLDSVGSFPLYSKLTVDKSRWQQGNVFCVMHEALHNHYQOQSLSLSEPK	232
Db	429	PVLDSGSFPLYSKLTVDKSRWQQGNVFCVMHEGLNHYTKQSLSLSLSEPK	480

Search completed: February 22, 2006, 21:37:12
Job time : 154.266 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:37:34 ; Search time 49.0155 seconds
(without alignments)
556.619 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGSEVPLAPSKSTSG.....MHEALHNYQKSLSPK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/prodata/1/iaa/H COMB.pep.*

4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*

5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1729	98.0	371	1 US-08-236-311-7	Sequence 7, Appli
2	1729	98.0	371	2 US-08-457-918-7	Sequence 7, Appli
3	1729	98.0	371	2 US-10-157-408-7	Sequence 7, Appli
4	1729	98.0	446	2 US-08-397-411-7	Sequence 7, Appli
5	1729	98.0	449	1 US-08-458-516-13	Sequence 13, Appli
6	1729	98.0	467	2 US-08-030-175-41	Sequence 41, Appli
7	1729	98.0	467	2 US-08-030-175-42	Sequence 42, Appli
8	1729	98.0	470	2 US-10-104-047-3730	Sequence 3730, Ap
9	1729	98.0	476	1 US-08-378-939-10	Sequence 10, Appli
10	1729	98.0	547	2 US-09-746-359A-54	Sequence 54, Appli
11	1729	98.0	567	2 US-09-746-561A-16	Sequence 16, Appli
12	1729	98.0	571	2 US-09-746-359A-53	Sequence 53, Appli
13	1729	98.0	951	2 US-09-313-942-9	Sequence 9, Appli
14	1729	98.0	951	2 US-10-282-162-9	Sequence 9, Appli
15	1729	97.8	462	2 US-09-289-942A-7	Sequence 7, Appli
16	1725	97.8	475	2 US-09-740-002-27	Sequence 27, Appli
17	1725	97.8	476	2 US-08-487-550-4	Sequence 4, Appli
18	1725	97.8	476	2 US-08-487-550-12	Sequence 12, Appli
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31	1725	97.8	478	2	US-09-576-424-8	Sequence 8, Appli
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33	1724	97.7	470	2	US-09-238-741-4	Sequence 4, Appli
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35	1723	97.7	330	2	US-09-301-593-22	Sequence 22, Appli
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37	1723	97.7	451	1	US-08-887-352B-14	Sequence 14, Appli
38	1723	97.7	451	1	US-08-887-352B-18	Sequence 18, Appli
39	1723	97.7	451	2	US-08-466-151-65	Sequence 65, Appli
40	1723	97.7	451	2	US-09-109-207C-14	Sequence 14, Appli
41	1723	97.7	451	2	US-09-109-207C-16	Sequence 16, Appli
42	1723	97.7	451	2	US-09-109-207C-18	Sequence 18, Appli
43	1723	97.7	451	2	US-09-282-505-2	Sequence 2, Appli
44	1723	97.7	451	2	US-09-054-255-2	Sequence 2, Appli
45	1723	97.7	451	2	US-09-296-005-14	Sequence 14, Appli

ALIGNMENTS

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RESULT 1
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

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US-08-236-311-7
Query Match      98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNWSGALTSGVHTTFAVLQSS 60
DB 42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNWSGALTSGVHTTFAVLQSS 101
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 120
DB 102 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 161
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 162 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 181 STYRVSVLTVLHQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 341
QY 301 QQGNVFSCSVMHEALHNHYQOQSLSLSPGK 330
DB 342 QQGNVFSCSVMHEALHNHYQOQSLSLSPGK 371

RESULT 2
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.

US-08-236-311-7
Query Match      98.0%; Score 1729; DB 2; Length 371;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNWSGALTSGVHTTFAVLQSS 60
DB 42 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNWSGALTSGVHTTFAVLQSS 101
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 120
DB 102 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 161
QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
DB 162 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 221
QY 181 STYRVSVLTVLHQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQWMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFFLYSKLTVDKSRW 341
QY 301 QQGNVFSCSVMHEALHNHYQOQSLSLSPGK 330
DB 342 QQGNVFSCSVMHEALHNHYQOQSLSLSPGK 371

RESULT 3
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
```


FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1998
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444PIC3
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-157-408-7

Query Match 98.0%; Score 1729; DB 2; Length 371;
Best Local Similarity 97.9%; Pred. No. 1.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNNGALTSVHTFPAVLQSS 60
DB 42 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNNGALTSVHTFPAVLQSS 101

QY 61 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPPELLGG 120
DB 102 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPPELLGG 161

QY 121 PSVFLPPPKDPTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 180
DB 162 PSVFLPPPKDPTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 221

QY 181 STYRVSVLTVLHQNWMNGEKYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQNWMNGEKYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 281

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 341

QY 301 QQGNVFCSCVMHEALHNNHYQKSLSPGK 330
DB 342 QQGNVFCSCVMHEALHNNHYQKSLSPGK 371

RESULT 4
US-08-397-411-7
Sequence 7, Application US/08397411
Patent No. 6129914
GENERAL INFORMATION:
APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-411-7

Query Match 98.0%; Score 1729; DB 2; Length 446;
Best Local Similarity 97.9%; Pred. No. 1.5e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNNGALTSVHTFPAVLQSS 60
DB 117 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVWSNNGALTSVHTFPAVLQSS 176

QY 61 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPPELLGG 120
DB 177 GLYSLSVVTVPSSSISLTQYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPPELLGG 236

QY 121 PSVFLPPPKDPTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 180
DB 237 PSVFLPPPKDPTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTPREEQYN 296

QY 181 STYRVSVLTVLHQNWMNGEKYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 297 STYRVSVLTVLHQNWMNGEKYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 356

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 357 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 416

QY 301 QQGNVFCSCVMHEALHNNHYQKSLSPGK 330
DB 417 QQGNVFCSCVMHEALHNNHYQKSLSPGK 446

RESULT 5
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: Co. Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/458,516
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/059,159
;; FILING DATE: 03-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-37-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 449 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;
Best Local Similarity 97.9%; Pred. No. 1.5e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGSPVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 120 ASTKGSPVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179

Qy 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 120
Db 180 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 239

Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 240 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 299

Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 300 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 359

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSFFLYSKLTVDKSRW 300
Db 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSFFLYSKLTVDKSRW 419

Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 420 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 449

RESULT 6
US-08-030-175-41
; Sequence 41, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.

;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
;; COMPUTER: IBM AT compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
;; SOFTWARE: WordPerfect 5.0 (Dos Text)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/030,175
;; FILING DATE: 17-MAY-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB91/01578
;; FILING DATE: 13-SEP-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ernst, Barbara G.
;; REGISTRATION NUMBER: 30,377
;; REFERENCE/DOCKET NUMBER: 1768-113
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)783-6040
;; TELEFAX: (202)783-6031
;; INFORMATION FOR SEQ ID NO: 41:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 467 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-030-175-41

Query Match 98.0%; Score 1729; DB 2; Length 467;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGSPVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 138 ASTKGSPVFLAPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197

Qy 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 120
Db 198 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 257

Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
Db 258 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317

Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 318 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 377

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSFFLYSKLTVDKSRW 300
Db 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGVSFFLYSKLTVDKSRW 437

Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 438 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 467

RESULT 7
US-08-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.

COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT compatible
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
SOFTWARE: WordPerfect 5.0 (Dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-030-175-42

Query Match 98.0%; Score 1729; DB 2; Length 467;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 138 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
QY 61 GLYSLSVVTVFSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 120
DB 198 GLYSLSVVTVFSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 257
QY 121 PSVFLPPPKKOTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 258 PSVFLPPPKKOTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 317
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 318 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 377
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 437
QY 301 QQGNVFCSCVMHEALHNNHYQQRSLSPGK 330
DB 438 QQGNVFCSCVMHEALHNNHYQQRSLSPGK 467

RESULT 8

US-10-104-047-3730
Sequence 3730, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3730

LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3730

Query Match 98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSVVTVFSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 120
DB 201 GLYSLSVVTVFSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 260
QY 121 PSVFLPPPKKOTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 261 PSVFLPPPKKOTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 320
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 321 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 440
QY 301 QQGNVFCSCVMHEALHNNHYQQRSLSPGK 330
DB 441 QQGNVFCSCVMHEALHNNHYQQRSLSPGK 470

RESULT 9

US-08-378-939-10
Sequence 10, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGS, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10

Query Match          98.0%; Score 1729; DB 1; Length 476;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
Db 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 206

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
Db 207 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 266

Qy 121 PSVFLFPPPKPDTLMIKSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 267 PSVFLFPPPKPDTLMIKSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 326

Qy 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db 327 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 386

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSKLTVDKSRW 300
Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSKLTVDKSRW 446

Qy 301 QQGNVFSCSVMEALHNNHYQORSLSLSPGK 330
Db 447 QQGNVFSCSVMEALHNNHYQORSLSLSPGK 476

RESULT 10
US-09-746-359A-54
; Sequence 54, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekhar, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

Query Match          98.0%; Score 1729; DB 2; Length 547;
Best Local Similarity 97.9%; Pred. No. 2e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
Db 218 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 277

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10

Query Match          98.0%; Score 1729; DB 1; Length 476;
Best Local Similarity 97.9%; Pred. No. 1.6e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
Db 278 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 337

Qy 121 PSVFLFPPPKPDTLMIKSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 338 PSVFLFPPPKPDTLMIKSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 397

Qy 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db 398 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 457

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSKLTVDKSRW 300
Db 458 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSKLTVDKSRW 517

Qy 301 QQGNVFSCSVMEALHNNHYQORSLSLSPGK 330
Db 518 QQGNVFSCSVMEALHNNHYQORSLSLSPGK 547

RESULT 11
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHALL CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalphallR/IgGgamma1 polypeptide
US-09-825-561A-16

Query Match          98.0%; Score 1729; DB 2; Length 567;
Best Local Similarity 97.9%; Pred. No. 2.1e-156;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
Db 238 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 297

Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
Db 298 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 357

Qy 121 PSVFLFPPPKPDTLMIKSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 358 PSVFLFPPPKPDTLMIKSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 417

Qy 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db 418 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 477

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSKLTVDKSRW 300
Db 478 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSKLTVDKSRW 537

```

QY 301 QOQNVFSCVMHEALHNHYOORSLSPGK 330
 Db 538 QOQNVFSCVMHEALHNHYTKLSLSPGK 567

RESULT 12

US-09-746-359A-53
 ; Sequence 53, Application US/09746359A
 ; Patent No. 6610286
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Penny
 ; APPLICANT: Foster, Donald C.
 ; APPLICANT: Xu, Wenfeng
 ; APPLICANT: Madden, Karen L.
 ; APPLICANT: Kelly, James D.
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Blumberg, Hal
 ; APPLICANT: Eagan, Maribeth A.
 ; APPLICANT: Jaspers, Stephen R.
 ; APPLICANT: Chandrasekhar, Yasmin A.
 ; APPLICANT: No. 6610286ak, Julia B.
 ; TITLE OF INVENTION: Method for Treating Inflammation
 ; FILE REFERENCE: 99-108
 ; CURRENT APPLICATION NUMBER: US/09/746,359A
 ; CURRENT FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/171,969
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: 60/213,341
 ; PRIOR FILING DATE: 2000-06-22
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 53
 ; LENGTH: 571
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-746-359A-53

Query Match 98.0%; Score 1729; DB 2; Length 571;
 Best Local Similarity 97.9%; Pred. No. 2.1e-156;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 Db 242 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 301
 QY 61 GLYSLSVVTVPPSSLSGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTCCPCPAPPELLGG 120
 Db 302 GLYSLSVVTVPPSSLSGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTCCPCPAPPELLGG 361
 QY 121 PSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 362 PSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 421
 QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
 Db 422 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 481
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFPLYSLKLTVDKSRW 300
 Db 482 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFPLYSLKLTVDKSRW 541
 QY 301 QOQNVFSCVMHEALHNHYOORSLSPGK 330
 Db 542 QOQNVFSCVMHEALHNHYTKLSLSPGK 571

RESULT 13

US-09-313-942-9
 ; Sequence 9, Application US/09313942
 ; Patent No. 6472179
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-A
 ; CURRENT APPLICATION NUMBER: US/09/313,942
 ; CURRENT FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 09/313,942
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: 60/101,858
 ; PRIOR FILING DATE: 1998-09-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 951
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-313-942-9

Query Match 98.0%; Score 1729; DB 2; Length 951;
 Best Local Similarity 97.9%; Pred. No. 4.6e-156;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 Db 622 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 681
 QY 61 GLYSLSVVTVPPSSLSGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTCCPCPAPPELLGG 120
 Db 682 GLYSLSVVTVPPSSLSGTQTYICNVNHPKPSNTKVDKVPKSCDKTHTCCPCPAPPELLGG 741
 QY 121 PSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
 Db 742 PSVFLPPPKPDTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 801
 QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
 Db 802 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 861
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFPLYSLKLTVDKSRW 300
 Db 862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFPLYSLKLTVDKSRW 921
 QY 301 QOQNVFSCVMHEALHNHYOORSLSPGK 330
 Db 922 QOQNVFSCVMHEALHNHYTKLSLSPGK 951

RESULT 14

US-10-282-162-9
 ; Sequence 9, Application US/10282162
 ; Patent No. 6927044
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-B-US
 ; CURRENT APPLICATION NUMBER: US/10/282,162
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/787,835
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 951
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-282-162-9

Query Match 98.0%; Score 1729; DB 2; Length 951;
 Best Local Similarity 97.9%; Pred. No. 4.6e-156;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db |||||||
Qy 622 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 681
Db |||||||
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 120
Db |||||||
Qy 682 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 741
Db |||||||
Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180
Db |||||||
Qy 742 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 801
Db |||||||
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db |||||||
Qy 802 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 861
Db |||||||
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db |||||||
Qy 862 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 921
Db |||||||
Qy 301 QQGNVFCSVMHEALHNHYQORSLSLSPGK 330
Db |||||||
Qy 922 QQGNVFCSVMHEALHNHYQORSLSLSPGK 951
Db |||||||
```

```
RESULT 15
US-09-289-942A-7
; Sequence 7, Application US/09289942A
; Patent No. 6482928
; GENERAL INFORMATION:
; APPLICANT: Pai, Emil F.
; APPLICANT: Klein, Michel H.
; APPLICANT: Chong, Pele
; APPLICANT: Pedyczak, Arthur
; TITLE OF INVENTION: Fab'-EPITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
; FILE OF INVENTION: MONOCLONAL ANTIBODY 2F5
; FILE REFERENCE: 1038-926 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/289,942A
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-289-942A-7
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Query Match 97.8%; Score 1725; DB 2; Length 462;
Best Local Similarity 97.6%; Pred. No. 3.7e-156;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db |||||||
Qy 133 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 192
Db |||||||
Qy 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 120
Db |||||||
Qy 193 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 252
Db |||||||
Qy 121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180
Db |||||||
Qy 253 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 312
Db |||||||
Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db |||||||
Qy 313 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 372
Db |||||||
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300
Db |||||||
Qy 373 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 432
Db |||||||
Qy 301 QQGNVFCSVMHEALHNHYQORSLSLSPGK 330
Db |||||||
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Db 433 QQGNVFCSVMHEALHNHYQORSLSLSPGK 462

Search completed: February 22, 2006, 21:39:48

Job time : 50.0155 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:11 ; Search time 216.58 Seconds
(without alignments)
669.475 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVFLAPLSKSTSG.....MHEALHHYQORSLSLSPCK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764	100.0	330	AA019664	AA019664 Human Igg
2	1732	98.2	330	ADZ69628	ADZ69628 Human Igg
3	1729	98.0	330	AAB04071	AAB04071 Zcytor 10
4	1729	98.0	330	AAW47856	AAW47856 Human Igg
5	1729	98.0	330	AAE21960	AAE21960 Human Igg
6	1729	98.0	330	ABB81641	ABB81641 Human Igg
7	1729	98.0	330	ABB05736	ABB05736 Human Igg
8	1729	98.0	330	ABP71856	ABP71856 Human Igg
9	1729	98.0	330	AAE32915	AAE32915 Human Igg
10	1729	98.0	330	AAE32627	AAE32627 Human Igg
11	1729	98.0	330	ABR82103	ABR82103 Human DR6
12	1729	98.0	330	AAO31102	AAO31102 Human A2-
13	1729	98.0	330	ABR55836	ABR55836 Anti-Ang-
14	1729	98.0	330	AAO30893	AAO30893 Human Igg
15	1729	98.0	330	ADF11389	ADF11389 Anti-OPGL
16	1729	98.0	330	ADSF7351	ADSF7351 Human Igg
17	1729	98.0	330	ADF83605	ADF83605 Cytokine
18	1729	98.0	330	ADF75001	ADF75001 Human Igg
19	1729	98.0	330	ADM41537	ADM41537 Anti-inte
20	1729	98.0	330	ADM68911	ADM68911 Human Igg
21	1729	98.0	330	ADR43460	ADR43460 Heavy cha
22	1729	98.0	330	ADR31605	ADR31605 Human Igg
23	1729	98.0	330	ADSF7909	ADSF7909 Anti-IFN-
24	1729	98.0	330	ADN33230	ADN33230 IgG1-CH h

25	1729	98.0	330	8	ADS94906	AdS94906 Anti-IFN-
26	1729	98.0	330	8	ADS33009	AdS33009 Human Igg
27	1729	98.0	330	8	ADT88869	AdT88869 Human Igg
28	1729	98.0	330	8	ADT51577	AdT51577 Heavy cha
29	1729	98.0	330	8	ADT51581	AdT51581 Heavy cha
30	1729	98.0	330	8	ADT51724	AdT51724 Human Igg
31	1729	98.0	330	8	ADU68015	AdU68015 Mouse ant
32	1729	98.0	330	9	ADW08868	AdW08868 IGF-IR an
33	1729	98.0	330	9	ADW86657	AdW86657 Human imm
34	1729	98.0	330	9	ADX97894	AdX97894 Human Igg
35	1729	98.0	330	9	ADX98273	AdX98273 Human ant
36	1729	98.0	330	9	ADY51253	AdY51253 Human Igg
37	1729	98.0	330	9	ADY58147	AdY58147 Human Igg
38	1729	98.0	330	9	ADY26687	AdY26687 Human ant
39	1729	98.0	330	9	AEA12531	AEa12531 Human Igg
40	1729	98.0	330	9	AEA25942	AEa25942 Human imm
41	1729	98.0	330	9	AEA48148	AEa48148 Human Igg
42	1729	98.0	330	9	AE86186	AEb6186 Amino aci
43	1729	98.0	330	9	AEC08181	AEc08181 Heavy cha
44	1729	98.0	332	8	ADL35095	AdL35095 Human Igg
45	1729	98.0	332	9	ADW07455	AdW07455 Human Igg

ALIGNMENTS

RESULT 1

AAO19664

ID AAO19664 standard; protein; 330 AA.

AC AAO19664;

DT 28-MAR-2003 (first entry)

DE Human IgG1 heavy chain constant region.

Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
Fc epsilon receptor; autoimmune disease; constant region; heavy chain;
antiaschmatic; antiallergic; antiinflammatory; dermatological;
antiarthritic; antirheumatic; antidiabetic; neuroprotective.

OS Homo sapiens.

PN WO200288317-A2.

PD 07-NOV-2002.

PF 01-MAY-2002; 2002WO-US013527.

PR 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

PA (REGC) UNIV CALIFORNIA.

PI Saxon A, Zhang K, Zhu D;

DR WPI; 2003-103456/09.

New fusion molecules comprising polypeptide sequences that bind to IgG
inhibitory receptor and native IGE receptor, useful for treating Ige-
mediated hypersensitivity reactions, e.g. asthma or allergies, or
autoimmune diseases.

PT Claim 64; Fig 2; 116pp; English.

The present invention relates to a fusion molecule comprising a first
polypeptide sequence capable of specific binding to a native Igg
inhibitory receptor consisting of an immune receptor tyrosine-based
inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
functionally connected to a second polypeptide sequence capable of
specific binding directly or indirectly to a native Ige receptor
(Fc epsilon receptor). Also provided are nucleotide sequences encoding such a
fusion protein. The fusion molecules and compositions are useful for

CC treating an IgE-mediated biological response, preferably an IgE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IgG1
CC heavy chain constant region
XX
SQ Sequence 330 AA;
Query Match 100.0%; Score 1764; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 4,6e-125;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCCPCPAPELLGG 120
Qy 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLYSLKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
RESULT 2
ADZ69628 standard; protein; 330 AA.
XX
AC ADZ69628;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human IgG1 heavy chain constant region, mutant L314M.
XX
KW Heavy chain constant region; antibody engineering; protein engineering;
KW immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasm;
KW autoimmune disease; immunosuppressive; immune disorder.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 197
FT /note= "Wild-type Leu substituted by Met"
XX
FN WO2005037867-A1.
XX
XX
PD 28-APR-2005.
XX
XX 15-OCT-2004; 2004WO-US034440.
XX
PR 15-OCT-2003; 2003US-0511687P.
PR 14-APR-2004; 2004US-0562627P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Hinton PR, Tsurushita N;

XX WPI; 2005-315683/32.
DR
XX New modified Fc-fusion protein where at least one amino acid residue from
PT the heavy chain constant region, useful for studying protein function in
PT vitro and in vivo and as potential therapeutic and diagnostic agents.
XX
PS Claim 21; SEQ ID NO 29; 170pp; English.
XX
CC The invention relates to a modified Fc-fusion protein where at least one
CC amino acid residue from the heavy chain constant region selected from
CC residues 250, 314, and 428 (Kabat numbering) is different from that
CC present in the unmodified Fc-fusion protein. Also included are an Fc-
CC fusion protein comprising an Fc region substantially identical to that of
CC a naturally occurring class IgG antibody, a modified Fc-fusion protein
CC with an in vivo mean elimination half-life at least about 1.3-fold longer
CC than that of the corresponding unmodified Fc-fusion protein, a modified
CC IgG class antibody fragment (comprising a heavy chain constant region or
CC Fc-region where at least one amino acid residue selected from the group
CC consisting of residues 250, 314, and 428 is different from that present
CC in the unmodified IgG class antibody), an isolated polynucleotide
CC molecule encoding a polypeptide comprising a sequence at least 90%
CC identical to a sequence selected from ADZ69600-ADZ69656, an isolated
CC polypeptide comprising an amino acid sequence at least 90% identical to a
CC sequence selected from ADZ69600-ADZ69656, a method for altering FcRn
CC binding affinity/serum half-life of an Fc-fusion protein (comprising
CC selecting at least one amino acid residue as cited above, and
CC substituting the selected residue(s) with an amino acid different from
CC that present in the Fc-fusion protein) and a method of producing a
CC modified Fc-fusion protein with an altered binding affinity for
CC FcRn/alterd serum half-life as compared with the unmodified Fc-fusion
CC protein (comprising preparing an expression vector comprising a suitable
CC promoter operably linked to DNA encoding at least a constant region of an
CC IgG heavy chain, transforming host cells with the vector and culturing
CC the transformed host cells to produce the modified IgG Fc fusion
CC protein). The modified antibody has a higher affinity for FcRn at pH 6.0
CC than at pH 8.0. The fusion proteins are useful for studying protein
CC function in vitro and in vivo and as potential therapeutic and diagnostic
CC agents. The present sequence represents a human IgG1 heavy chain constant
CC region with an amino acid substitution at residue 250, 314 or 428 (Kabat
CC numbering, the actual residue that is mutated is covered in the feature
CC table).
XX
SQ Sequence 330 AA;
Query Match 98.2%; Score 1732; DB 9; Length 330;
Best Local Similarity 98.2%; Pred. No. 1.2e-122;
Matches 324; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Db 1 ASTKGPSVFPFLAPSSKSTSGTAAAGCLVKDYFPEPTVSMNSGALTSVHTFPAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHCCPCPAPELLGG 120
Qy 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLYSLKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLYSLKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 3
 AAB04071
 ID AAB04071 standard; protein; 330 AA.
 XX
 AC AAB04071;
 XX
 DT 11-APR-2001 (first entry)
 XX
 XX Zcytor 10::IGG gamma fusion peptide.
 XX
 DE zcytor 10 cytokine receptor; cytokine; receptor; antibody; ligand;
 XX KW binding; detection; modulation; recombinant cell; haematopoietic cell;
 KW lymphoid cell; myeloid cell; lymph; immune system; blood; bone;
 KW inflammatory response; inflammation; spleen; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200068381-A1.
 XX
 XX 16-NOV-2000.
 XX
 XX 11-MAY-2000; 2000WO-US012924.
 PF
 XX 11-MAY-1999; 99US-00309861.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Presnell SR, Foster DC, Hammond AK, Lok S;
 PI
 XX WPI; 2001-016096/02.
 DR
 DR N-PSDB; AAA54473.
 XX
 XX New cytokine receptor mouse zcytor 10, useful for detecting ligands that
 PT stimulate proliferation or development of hematopoietic, lymphoid and
 PT myeloid cells.
 XX
 XX Example 17; Page 120-121; 134pp; English.
 PS
 XX Isolating a nucleotide which encodes the zcytor 10 cytokine receptor
 CC enables the production of recombinant cells expressing the receptor.
 CC Those cells can then be used to detect the presence of a modulator of
 CC zcytor10 protein by culturing the cells in the presence of a test ligand
 CC and comparing levels of activity of mouse zcytor10 in the presence and
 CC absence of the test sample. Similarly, detection of zcytor10 receptor
 CC ligand within a test sample can be achieved. The method comprising
 CC contacting a test sample containing an amino acid sequence from Cys15 or
 CC Gly25 to Pro230 of the zcytor 10 cytokine receptor and detecting the
 CC binding of the polypeptide to a ligand in the sample. Specified peptide
 CC fragments of the zcytor 10 cytokine receptor and the methods described
 CC are used to identify ligands that stimulate the proliferation and/or
 CC development of haematopoietic, lymphoid and myeloid cells. Peptide
 CC fragments of the cytokine receptor are useful for treating lymphoid,
 CC immune, inflammatory, splenic, blood or bone disorders and for generating
 CC antibodies directed against the receptor. A vector expressing a secreted
 CC human zcytor 10 heterodimer is constructed. In this construct the
 CC extracellular cytokine binding domain of zcytor 10 is fused to the heavy
 CC chain of Igg gamma and the extracellular portion of the heteromeric
 CC cytokine receptor subunit (an interleukin receptor subunit) is fused to
 CC human kappa light chain (See GENESEQ record AAA54474). The two sequences
 CC are fused together using two primers (AAA54475, AAA54476)
 XX
 XX Sequence 330 AA;
 SQ
 Query Match 98.0%; Score 1729; DB 4; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYKPEPVTVSWNSGALTSGVHPFPAVLQSS 60
 DB 1 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYKPEPVTVSWNSGALTSGVHPFPAVLQSS 60

61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNTPKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
 |||||
 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNTPKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
 |||||
 121 PSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
 |||||
 121 PSVFLPPPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
 |||||
 181 STYRVVSVLTVLHQNMMGKEYKCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
 |||||
 181 STYRVVSVLTVLHQNMMGKEYKCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
 |||||
 241 LTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 |||||
 241 LTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 |||||
 301 QQGNVPSCSVMEALHNHYQOQSLSLSPGK 330
 |||||
 301 QQGNVPSCSVMEALHNHYQOQSLSLSPGK 330
 |||||

RESULT 4
 AAM47856
 ID AAM47856 standard; protein; 330 AA.
 XX
 AC AAM47856;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Human Ig-gammal heavy chain constant region amino acid sequence.
 XX
 KW Human; immunoadhesin; intercellular adhesion molecule; ICAM-1;
 KW human rhinovirus; immunoglobulin heavy chain; J chain; HRV; common cold;
 KW transgenic plant.
 XX
 OS Homo sapiens.
 XX
 PN WO200183529-A2.
 XX
 XX 08-NOV-2001.
 PD
 XX 28-APR-2001; 2001WO-US013932.
 PF
 XX 28-APR-2000; 2000US-0200298P.
 PR
 XX (PLAN-) PLANET BIOTECHNOLOGY INC.
 PA
 XX Larrick JW, Wycoff KL;
 PI WPI; 2002-041481/05.
 DR N-PSDB; ABA05265.
 XX
 XX Immunoadhesin for treating human rhinovirus infection comprises chimeric
 PT intercellular adhesion molecule-1, and optionally a J chain and secretory
 PT component in association.
 XX
 PS Disclosure; Fig 7; 138pp; English.
 XX
 XX The invention relates to an immunoadhesin comprising: (a) a chimeric
 CC intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor
 CC protein linked to at least a portion of an immunoglobulin heavy chain;
 CC and (b) optionally a J chain and secretory component associated with the
 CC chimeric ICAM-1 molecule. The immunoadhesin has plant-specific
 CC glycosylation and virucide activity. The immunoadhesin is useful for
 CC reducing infection by human rhinovirus (HRV) and hence the initiation or
 CC spread of the common cold by HRV. The immunoadhesin binds to HRV and
 CC reduces its infectivity, competing with cell surface ICAM-1 for binding
 CC sites, interfering with virus entry or coating and directing premature
 CC release of viral RNA and formation of empty capsids. Expression of the
 CC immunoadhesin in plants would be tetrameric, rather than dimeric.
 CC Immunoadhesin having multiple binding sites have a higher effective
 CC affinity for the virus, thereby increasing the effectiveness of the
 CC immunoadhesin. Association of secretory component and immunoglobulin J

CC chain increases the stability of the immunoadhesin in the mucosal
 CC environment. Production is significantly less expensive in plants than in
 CC animal cell culture and production in plants is safer for human use,
 CC since plants are not known to harbor any animal viruses. The present
 CC sequence is that of a human immunoglobulin protein sequence, useful to
 CC the invention
 XX
 XX
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTSGVHTTFAVQLSS 60
 Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTSGVHTTFAVQLSS 60
 Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCCPAPPELLGG 120
 Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCCPAPPELLGG 120
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNVTKPREPQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNVTKPREPQYN 180
 Qy 181 STYRVSVTLVTLHONMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
 Db 181 STYRVSVTLVTLHONMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
 Qy 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330
 Db 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330

RESULT 5
 AAEE21960
 ID AAE21960 standard; protein; 330 AA.
 AC AAE21960;
 XX
 XX 25-JUL-2002 (first entry)
 XX Human death domain containing receptor (DR6) protein-related protein.
 XX Human; therapy; death domain containing receptor; DR6; receptor; anaemia;
 XX apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;
 XX diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;
 XX transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;
 XX autoimmune; gastritis; dermatosis; cardiopathy; infertility; haemostatic;
 XX H. pylori-associated ulceration; anti-inflammatory; vasotropic; virucide;
 XX acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;
 XX HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;
 XX adult respiratory distress syndrome; ARDS; cycostatic; thyromimetic;
 XX dermatological; hepatotropic; antibacterial.
 XX Homo sapiens.
 XX WO200185209-A2.
 XX
 XX 15-NOV-2001.
 XX
 XX 30-APR-2001; 2001WO-US011735.
 XX
 XX 10-MAY-2000; 2000US-0203015P.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX Heuer JG, Liu J, Na S, Song HY, Yang D;
 XX

DR WPI; 2002-351283/38.
 XX Treating or preventing T cell or Th2 cell mediated condition e.g., asthma
 PT or multiple sclerosis in mammal, comprises administering composition
 PT comprising death domain containing receptor, DR6 agonist or antagonist.
 XX
 PS Disclosure; Page 132-133; 133pp; English.

CC The invention relates to a method for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. The
 CC method comprising administering to the mammal a pharmaceutical
 CC composition comprising a death domain containing receptor (DR6) agonist
 CC or antagonist. The method is useful for treating or preventing a T cell
 CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6
 CC agonist is useful in the manufacture of a medicament for treating or
 CC preventing at least one symptom associated with aberrant apoptosis, graft
 CC -versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy,
 CC inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-
 CC dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's
 CC thyroiditis, Graves disease, transplant rejection, systemic lupus
 CC erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune
 CC infertility, Behcet's disease, autoimmune gastritis, fibrosing lung
 CC disease, organ rejection after transplantation, thrombotic
 CC thrombocytopenic purpura (TTP), chronic glomerulonephritis, haemolytic
 CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ
 CC dysfunction syndrome (MODS), adult respiratory distress syndrome (ARDS)
 CC or a condition or symptom related to the above mentioned diseases in a
 CC mammal. An DR6 antagonist is useful in the manufacture of a medicament
 CC for treating or preventing at least one symptom associated with
 CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial
 CC infection, complications of infection, human immunodeficiency virus
 CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency
 CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis
 CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori
 CC associated ulceration, cytoprotection during cancer treatment,
 CC recuperation from chemotherapy, recuperation from irradiation therapy, or
 CC a condition or symptom related to the above mentioned diseases in a
 CC mammal. The present sequence is human DR6 protein-related protein
 XX
 XX Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTSGVHTTFAVQLSS 60
 Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTSGVHTTFAVQLSS 60
 Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCCPAPPELLGG 120
 Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCCPAPPELLGG 120
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNVTKPREPQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNVTKPREPQYN 180
 Qy 181 STYRVSVTLVTLHONMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
 Db 181 STYRVSVTLVTLHONMNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDVSGSFYFLSKLTVDKSRW 300
 Qy 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330
 Db 301 QQGNVFSCSVNHEALHNHYQOQSLSLSPGK 330

RESULT 6
 ABB81641
 ID ABB81641 standard; protein; 330 AA.

XX
AC ABB81641;
CC
DT 25-SEP-2002 (first entry)
XX
DE Human IgG gamma 1 heavy chain SEQ ID NO:15.
XX
KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
KW antirheumatic; antiarthritic; neuroprotective; anti-inflammatory;
KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;
KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
KW mesangioliferative disease; chronic lymphocytic leukaemia; bronchitis;
KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;
KW emphysema; chronic airway disease.
XX
OS Homo sapiens.
XX
XX WO200244209-A2.
XX
XX 06-JUN-2002.
XX
XX 28-NOV-2001; 2001WO-US044808.
XX
XX 28-NOV-2000; 2000US-0253561P.
PR 07-FEB-2001; 2001US-0267211P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;
XX
XX WPI: 2002-527700/56.
DR N-PSDB; ABQ73076.
XX
XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating
PT immune responses in animals for producing antibodies, and for treating
PT autoimmune diseases, leukemia and asthma.
XX
XX Example 7; Page 171-172; 200pp; English.
XX
XX The present invention describes an isolated human zcytor19 protein (I),
CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
CC antirheumatic, antiarthritic, neuroprotective, anti-inflammatory,
CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
CC activities, and can be used in vaccines. (I) or an antibody binding (I)
CC can be used for suppressing the immune system for reducing rejection of
CC tissue or organ transplants and grafts and for treating T-cell specific
CC leukaemias or lymphomas and autoimmune diseases including rheumatoid
CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
CC disease and Crohn's disease. The antibodies can also be used for treating
CC immunologic renal diseases, glomerulonephritis, mesangioliferative
CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
CC antibodies can also be used for renal or urological neoplasms and
CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway
CC diseases. Human zcytor19 is located to chromosome 1, more specifically to
CC chromosome 1p36.11. The present sequence represents a human IgG gamma 1
CC heavy chain protein, which is used in an example from the present
CC invention
XX
XX Sequence 330 AA;
SQ
Query Match 98.0%; Score 1729; DB 5; Length 330;
Best Local Similarity 97.9%; Pred. NO. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
1 ASTKGSPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60
1 ASTKGSPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60

61 GLYSLSVVTVTPSSSLGTQYICNVNHPKSNTKVDKVKPEKSCDKHTKCPCPAPPELLGG 120
61 GLYSLSVVTVTPSSSLGTQYICNVNHPKSNTKVDKVKPEKSCDKHTKCPCPAPPELLGG 120
121 PSVFLFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
121 PSVFLFPKPKDQTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
181 STYRVSVLTIVLHQNMMGKEYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
181 STYRVSVLTIVLHQNMMGKEYCKVSNKALPAPIEKTIISKAKVQPREPOVYTLPPSRDE 240
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVSGFSLYSLKTVDKSRW 300
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVSGFSLYSLKTVDKSRW 300
301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 7
ABB05736
ID ABB05736 standard; protein; 330 AA.
XX
AC ABB05736;
XX
DT 01-MAY-2002 (first entry)
XX
DE Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.
XX
KW Zcytor17; chromosome 5; 5q11; cytokine receptor; immunomodulatory;
KW antinflammatory; antiviral; antirheumatic; antiarthritic; cytostatic;
KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;
KW infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
KW inflammatory disease; pancreatitis; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
XX WO200200721-A2.
XX
XX 03-JAN-2002.
XX
XX 26-JUN-2001; 2001WO-US020484.
XX
XX 26-JUN-2000; 2000US-0214282P.
PR 29-JUN-2000; 2000US-0214955P.
PR 08-FEB-2001; 2001US-0267963P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL;
PI Maurer MF;
XX
XX WPI: 2002-090519/12.
XX
XX N-PSDB; ABA93797.
XX
XX Isolated polynucleotide encoding a cytokine receptor zcytor17 which is
PT useful for treating and diagnosing lymphoid, immune, inflammatory,
PT splenic, blood or bone disorders.
XX
XX Example 17; Page 187-188; 235pp; English.
XX
XX The present invention describes a cytokine receptor designated zcytor17.
CC Zcytor17 has immunomodulatory, antinflammatory, antiviral, cytostatic,
CC antirheumatic, antiarthritic and muscular activities. The zcytor17
CC proteins are useful for treating and diagnosing lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. Agonists or anti-
CC zcytor17 antibodies are useful in stimulating cell-mediated immunity and
CC for stimulating lymphocyte proliferation, such as in the treatment of
CC infections involving immunosuppression, including certain viral

CC infections. They are also useful for inducing cytotoxicity and for
 CC treating leukopenias. Antagonist of zcytor17 polypeptides are useful for
 CC treating autoimmune diseases (e.g. rheumatoid arthritis and multiple
 CC sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer,
 CC pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to
 CC chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to
 CC ABA93843 and ABB05730 to ABB05745 represent sequences used in the
 CC exemplification of the present invention

XX SQ Sequence 330 AA;
 Query Match 98.0%; Score 1729; DB 5; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVWTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTCCPCPAPPELLGG 120
 DB 61 GLYSLSVWTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTCCPCPAPPELLGG 120
 QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 DB 121 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 QY 181 STYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
 QY 301 QQGNVFCSCVMHEALHNNHYQORSLSLSPGK 330
 DB 301 QQGNVFCSCVMHEALHNNHYQKSLSLSPGK 330

RESULT 8
 ABP71856
 ID ABP71856 standard; protein; 330 AA.
 XX
 AC ABP71856;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE Human IgG1 Fc gamma region.
 XX
 KW Human; fusion protein; IgE Fc epsilon; IgG Fc gamma; Fc epsilon; allergy;
 KW Fc epsilon; Fc gamma; protein therapy; IgE; IgG; asthma; hay fever;
 KW allergic asthma; allergic rhinitis; hay fever; food allergy;
 KW atopic dermatitis; drug allergy; peanut allergen.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 1..98
 FT Region /label= CH1 region
 FT Region 99..113
 FT Region /label= Hinge region
 FT Region 114..223
 FT Region /label= CH2 region
 FT Region 224..330
 FT Region /label= CH3 region

XX WO2002102320-A2.
 XX 27-DEC-2002.
 XX 14-JUN-2002; 2002WO-US019448.
 XX

PR 15-JUN-2001; 2001US-0298710P.
 XX (TANO-) TANOX INC.
 XX
 PI An L, Wu H, Fung MSC;
 XX WPI; 2003-167440/16.
 XX
 PT New fusion protein which binds to Fc epsilonRI or RII receptor and
 PT Fc gammaRIIb receptor, useful for treating or preventing allergies and
 PT asthma, comprises an IgE Fc epsilon fragment and an IgG Fc gamma fragment.
 XX Disclosure; Fig 5; 32pp; English.
 XX
 CC The invention relates to a novel fusion protein comprising an IgE
 CC Fc epsilon fragment and an IgG Fc gamma fragment, which binds to an
 CC Fc epsilonRI and/or Fc epsilonRII receptor and an Fc gammaRIIb receptor. The
 CC fusion protein of the invention may have a use in protein therapy. The
 CC fusion protein is useful in treating or preventing IgE-mediated allergies
 CC and asthma, such as allergic asthma, allergic rhinitis, hay fever, food
 CC allergy, atopic dermatitis and drug allergy. The present sequence represents
 CC particularly caused by peanut allergen. The present sequence represents
 CC the human IgG1 Fc gamma fragment
 XX
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 1 ASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 QY 61 GLYSLSVWTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTCCPCPAPPELLGG 120
 DB 61 GLYSLSVWTVVPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKHTCCPCPAPPELLGG 120
 QY 121 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 DB 121 PSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 QY 181 STYRVSVLTVLHQNWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 DB 181 STYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
 QY 301 QQGNVFCSCVMHEALHNNHYQORSLSLSPGK 330
 DB 301 QQGNVFCSCVMHEALHNNHYQKSLSLSPGK 330

RESULT 9
 AAE32915
 ID AAE32915 standard; protein; 330 AA.
 XX
 AC AAE32915;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.
 XX
 KW T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1.
 XX
 OS Homo sapiens.
 XX
 FN WO200279232-A2.
 XX
 PD 10-OCT-2002.
 XX

```
PF 30-MAR-2002; 2002WO-US0009815.
XX
PR 30-MAR-2001; 2001US-0280625P.
XX
PA (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD;
XX
DR WPI; 2003-103259/09.
XX
XX
PT Reducing the immunogenicity of a fusion protein comprises changing an
PT amino acid within the junction region to reduce the ability of the
PT candidate T-cell epitope identified within the junction spanning to
PT interact with T-cell receptor.
XX
XX Disclosure; Page 49-50; 68pp; English.
PS
XX The invention relates to a method for reducing the immunogenicity of a
XX fusion protein which involves identifying a candidate T-cell epitope
XX within a junction spanning a fusion junction of a fusion protein, and
XX changing an amino acid within the junction region to reduce the ability
XX of the candidate T-cell epitope to interact with a T-cell receptor. The
XX method is useful for reducing the immunogenicity of a fusion protein. It
XX is useful for analysing, changing or modifying one or more amino acids in
XX the junction region of a fusion protein to identify a T-cell epitope and
XX reduce its ability to interact with a T-cell receptor. The less
XX immunogenic fusion proteins are useful in providing therapeutic
XX treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy
XX chain Fc region used to illustrate the method of the invention
XX
SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGSPVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGSPVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
QY 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVHREALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVHREALHNHYTQKSLSLSPGK 330
RESULT 10
AAE32627
ID AAE32627 standard; protein; 330 AA.
XX
AC AAE32627;
XX
XX 24-MAR-2003 (first entry)
XX
XX Human immunoglobulin G1 (IgG1) heavy chain Fc region.
XX
XX Human; immunogenic; therapy; immunoglobulin G1; IgG1.
XX
```

```
OS Homo sapiens.
XX
PN WO200279415-A2.
XX
PD 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US0009650.
XX
PR 30-MAR-2001; 2001US-0280625P.
XX
XX (LEXI-) LEXIGEN PHARM CORP.
XX
PI Gillies SD;
XX
DR WPI; 2003-111794/10.
XX
XX Reducing the immunogenicity of a fusion protein by changing an amino acid
XX within the junction region spanning a fusion junction of a fusion protein
XX to reduce the ability of the candidate T-cell epitope to interact with a
XX T-cell receptor.
XX
XX Disclosure; Page 49-50; 67pp; English.
XX
XX The present invention relates to a method of reducing the immunogenicity
XX of a fusion protein. The method involves identifying a candidate T-cell
XX epitope within a junction region spanning a fusion junction of a fusion
XX protein and changing an amino acid within the junction region to reduce
XX the ability of the candidate T-cell epitope to interact with a T-cell
XX receptor. The method is useful for reducing the immunogenicity of fusion
XX proteins for use in therapy. The present sequence is human immunoglobulin
XX G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the
XX method of the invention
XX
SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGSPVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGSPVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPSSSISLGTQYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120
QY 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVHREALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVHREALHNHYTQKSLSLSPGK 330
RESULT 11
ABR82103
ID ABR82103 standard; protein; 330 AA.
XX
AC ABR82103;
XX
XX 23-SEP-2003 (first entry)
XX
XX Human DR6 related amino acid sequence SEQ ID NO:5.
```

XX	Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;
KW	antiarthritic; antiasthmatic; dermatological; antiinflammatory;
KW	antipsoriatic; antidiabetic; cytostatic; neuroprotective; thyromimetic;
KW	antithyroid; nephrotropic; antiferility; vasotropic; virucide;
KW	hepatotropic; antibacterial; antiulcer; haemostatic; antianemic;
XX	antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.
XX	
OS	homo sapiens.
OS	
PN	WO2003051290-A2.
XX	
PD	26- JUN- 2003.
XX	
PF	10- DEC- 2002; 2002WO-US037596.
XX	
PR	17- DEC- 2001; 2001US-0342632P.
XX	
PA	(ELIL) LILLY & CO ELI.
XX	
PI	Liu J, Na S, Song HY, Yang D;
XX	
DR	WPI; 2003-541604/51.
XX	
PT	Treating or preventing a B cell mediated condition e.g., chronic
PT	hepatitis or chronic cirrhosis, in a mammal by administering a
PT	pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to
PT	the mammal.
XX	
PS	Disclosure; Page 96-97; 97pp; English.
XX	
CC	The present invention describes a method (M1) for treating or preventing
CC	a B cell mediated condition in a mammal by administering a pharmaceutical
CC	composition comprising a DR6 agonist or DR6 antagonist to the mammal.
CC	Also described: (1) Inhibiting B cell mediated immunity in a mammal, by
CC	administering a pharmaceutical composition comprising at least one DR6
CC	agonist; (2) use of a DR6 agonist in the manufacture of a medicament for
CC	treating or preventing at least one symptom associated with conditions
CC	(C1) such as aberrant apoptosis, graft-versus-host disease (GVHD), atopy,
CC	rheumatoid arthritis, asthma, eczema, inflammatory bowel disease, cancer,
CC	vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancreatitis,
CC	psoriasis, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease,
CC	transplant rejection, systemic lupus erythematosus, Behcet's disease,
CC	autoimmune nephropathy, autoimmune haematopathy, idiopathic interstitial
CC	pneumonia, hypersensitivity pneumonitis, autoimmune dermatosis,
CC	autoimmune cardiopathy, autoimmune infertility, autoimmune gastritis,
CC	fibrosing lung disease, fulminant viral hepatitis B, fulminant viral
CC	hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
CC	Helicobacter pylori-associated ulceration, organ rejection after
CC	transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic
CC	purpura (TTP) and haemolytic uraemic syndrome (HUS), aplastic anaemia,
CC	myelodysplasia, multiple organ dysfunction syndrome (MDS), adult
CC	respiratory distress syndrome (ARDS), and at least one condition or
CC	symptom related to the conditions, in a mammal; and (3) use of DR6
CC	antagonist in the manufacture of a medicament for treating or preventing
CC	at least one symptom associated with conditions (C2) such as aberrant
CC	apoptosis, immunodeficiency, bacterial infection, viral infection,
CC	microbial infection, complications of infection, HIV, HIV-induced
CC	lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral
CC	hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,
CC	H. pylori-associated ulceration, cytoprotection during cancer treatment,
CC	recuperation from chemotherapy, recuperation from irradiation therapy,
CC	and at least one condition or symptom related to the conditions, in a
CC	mammal. DR6 has immunosuppressive, antirheumatic, antiarthritic,
CC	antiasthmatic, dermatological, antiinflammatory, antipsoriatic,
CC	antidiabetic, cytostatic, neuroprotective, thyromimetic, antithyroid,
CC	nephrotropic, antiferility, vasotropic, virucide, hepatotropic,
CC	antibacterial, antiulcer, haemostatic, antianemic, antimicrobial and
CC	anti-HIV activities. (M1) is useful for treating or preventing at least
CC	one symptom associated with (C1) in a mammal, preferably human, by
CC	administering DR6 agonist, and for treating or preventing at least one
CC	symptom associated with (C2) by administering DR6 antagonist. The present
CC	sequence represents a human DR6 related amino acid sequent which is

CC	given in the exemplification of the present invention	
XX		
SQ	Sequence 330 AA;	
	Query Match 98.0%; Score 1729; DB 6; Length 330;	
	Best Local Similarity 97.9%; Pred. No. 2e-122;	
	Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
QY	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60	
DB	1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60	
QY	61 GLYSLSVVTVPPSSSLGTQTVICNNHKPSNTKVDKVKPEKSCDKTHTCPCPAPELLGG 120	
DB	61 GLYSLSVVTVPPSSSLGTQTVICNNHKPSNTKVDKVKPEKSCDKTHTCPCPAPELLGG 120	
QY	121 PSVFELPPPKDPTLMISPTPEVTCVVVDVSHEDDEVKFNWVVGVEVHNVTKPREEQYN 180	
DB	121 PSVFELPPPKDPTLMISPTPEVTCVVVDVSHEDDEVKFNWVVGVEVHNVTKPREEQYN 180	
QY	181 STYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240	
DB	181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240	
QY	241 LTKNQVSLTCLVKGYFPSDIAVEVESNGQPENNYKTTTPVLDVSGSPFLYSKLTVDKSRW 300	
DB	241 LTKNQVSLTCLVKGYFPSDIAVEVESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW 300	
QY	301 QQGNVFSCSVMHEALHNHYQOQSLSLSPGK 330	
DB	301 QQGNVFSCSVMHEALHNHYTKQSLSPGK 330	
RESULT 12		
AAO31102		
ID	AAO31102 standard; protein; 330 AA.	
XX		
AC	AAO31102;	
XX		
DT	06-OCT-2003 (first entry)	
XX		
DE	Human A2-G8 SCF antibody heavy chain constant region.	
XX		
KW	Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;	
KW	steel factor; c-kit ligand; gene therapy; heavy chain.	
XX		
OS	Homo sapiens.	
XX		
FN	WO2003051311-A2.	
XX		
PD	26-JUN-2003.	
XX		
PF	16-DEC-2002; 2002WO-US040227.	
XX		
PR	17-DEC-2001; 2001US-0342174P.	
XX		
PA	(FARB) BAYER CORP.	
XX		
PI	Takeuchi T, Tomkinson A, Neben S;	
XX		
DR	WPI; 2003-523500/49.	
DR	N-PSDB; AAL62618.	
XX		
PT	New purified human antibody that binds to stem cell factor protein,	
PT	useful for preparing a composition for treating asthma.	
XX		
PS	Example 10; Page 47-48; 94pp; English.	
XX		
CC	The invention provides human antibodies that bind to stem cell factor	
CC	(SCF) protein. SCF is also known as mast cell growth factor, steel factor	
CC	or c-kit ligand. Antibodies of the invention are useful for preparing The	
CC	compositions for treating asthma. They are also used in gene therapy. The	
CC	present sequence is human SCF antibody heavy chain constant region	

XX SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QQGNVFSCSVHAEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVHAEALHNHYTQKSLSLSPGK 330
RESULT 13
ID ABR55836 standard; protein; 330 AA.
XX ABR55836;
XX 02-SEP-2003 (first entry)
XX Anti-Ang-2 antibody IgG1 constant region.
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW Gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody; human.
OS Homo sapiens.
XX WO2003030833-A2.
XX 17-APR-2003.
XX 11-OCT-2002; 2002WO-US032613.
XX 11-OCT-2001; 2001US-0328604P.
PR 10-OCT-2002; 2002US-00269805.
XX (AMGE-) AMGEN INC.
XX Olinar JD;
XX WPI; 2003-504963/47.
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX Example 4; Page 96; 161pp; English.
XX The invention relates to a specific binding agent, which comprises at
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC fragment. The binding agents are antibodies that recognize and bind to
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the

CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity,
CC haemangioma, arteriosclerosis, endometriosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a human IgG1 constant region of an anti-Ang-2
CC antibody
XX SQ Sequence 330 AA;
Query Match 98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2e-122;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNMNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 301 QQGNVFSCSVHAEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVHAEALHNHYTQKSLSLSPGK 330
RESULT 14
ID AAO30893 standard; protein; 330 AA.
XX AAO30893;
XX 22-SEP-2003 (first entry)
XX Human immunoglobulin gamma (IgG) 1 constant region.
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; human.
OS Homo sapiens.
XX WO2003048334-A2.
XX 12-JUN-2003.
XX 04-DEC-2002; 2002WO-US038780.
XX 04-DEC-2001; 2001US-0337113P.
PR 12-APR-2002; 2002US-0371966P.
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX Gillies SD;
XX WPI; 2003-513757/48.
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT moiety, useful for preparing a composition for treating cancer, viral

PT infections or immune disorders.
 XX Example 1; Page 51-53; 71pp; English.
 XX The invention relates to cytokine fusion proteins with increased
 CC therapeutic index and methods for increasing the therapeutic index of
 CC such fusion proteins. The fusion protein comprises a non-interleukin-2
 CC (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a
 CC composition for treating cancer, viral infections or immune disorders.
 CC The fusion protein is also used in gene therapy. The present sequence is
 CC human immunoglobulin gamma (IgG) constant region. This sequence is used
 CC to illustrate the method of the invention
 XX Sequence 330 AA;
 SQ
 Query Match 98.0%; Score 1729; DB 6; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Qy 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Db 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQYN 180
 Qy 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
 Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 15
 ID ADF11389
 XX ADF11389 standard; protein; 330 AA.
 AC ADF11389;
 XX ADF11389;
 DT 12-FEB-2004 (first entry)
 DE Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.
 KW human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 OS Homo sapiens.
 XX WO2003086289-A2.
 PN 23-OCT-2003.
 XX 07-APR-2003; 2003WO-US010749.
 XX 05-APR-2002; 2002US-0370407P.
 XX (AMGE-) AMGEN INC.
 XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 XX WPI, 2003-845253/78.
 DR

DR N-PSDB; ADF11388.
 XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.
 XX Example 3; SEQ ID NO 2; 156pp; English.
 XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX Sequence 330 AA;
 SQ

Query Match 98.0%; Score 1729; DB 7; Length 330;
 Best Local Similarity 97.9%; Pred. No. 2e-122;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
 Qy 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Db 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPCPAPELGG 120
 Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQYN 180
 Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQYN 180
 Qy 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 Db 181 STYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
 Qy 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
 Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

Search completed: February 22, 2006, 21:30:43
 Job time : 220.58 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:31:15 ; Search time 33.6269 Seconds
(without alignments)
944.229 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGPSVFLAPSSKSTSG.....MHEALHNHYQORSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1729	98.0	330	1 GHU	Ig gamma-1 chain C
2	1592.5	90.3	377	2 A23511	Ig gamma-3 chain C
3	1590.5	90.2	377	2 A60764	Ig gamma-3 chain C
4	1566	88.8	326	1 G2HU	Ig gamma-2 chain C
5	1552.5	88.0	377	1 G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374	2 S69339	Ig heavy chain V r
7	1225	69.4	328	2 I47159	Ig gamma 2a chain
8	1222	69.3	255	4 S31866	Ig gamma-1 chain C
9	1219	69.1	328	2 I47160	Ig gamma 2b chain
10	1216	68.9	234	2 PT0207	Ig gamma chain C r
11	1193	67.6	328	2 I47158	Ig gamma 1 chain C
12	1192.5	67.6	323	1 GHRB	Ig gamma chain C r
13	1189	67.4	328	2 I47161	Ig gamma 3 chain C
14	1174.5	66.6	329	1 G2GP	Ig gamma-2 chain C
15	1163.5	66.0	472	2 S31459	Ig gamma-1 chain -
16	1144.5	64.9	470	2 S22080	Ig heavy chain pre
17	1125.5	63.8	308	2 C30554	Ig heavy chain C r
18	1123	63.7	289	1 G3HUW1	Ig gamma-3 heavy c
19	1117.5	63.4	333	2 PS0018	Ig gamma-2b chain
20	1116	63.3	444	2 PC4436	monoclonal antibod
21	1114	63.2	326	2 PS0017	Ig gamma-1 chain C
22	1109	62.9	324	1 G1MS	Ig gamma-1 chain C
23	1108	62.8	329	1 G3MSC	Ig gamma-1 chain C
24	1104	62.6	333	1 G1MSM	Ig gamma-1 chain C
25	1097	62.2	398	1 G3MSM	Ig gamma-3 chain C
26	1093	62.0	330	1 G2MSA	Ig gamma-2a chain
27	1093	62.0	469	2 S37483	Ig gamma-2a chain
28	1090.5	61.8	335	1 G2MSAB	Ig gamma-2a chain
29	1088	61.7	399	1 G2MSAM	Ig gamma-2a chain

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370

A;Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,

A;Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequ

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Content: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96, 'R', 98-135 <CUN>

A;Cross-references: UNIPARC:UPI000017378D

A;Note: this sequence has the Gln(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequ

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Accession: Eu

A;Content: Eu

A;Molecule type: protein

A;Residues: 136-154, 'O', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240

A;Cross-references: UNIPARC:UPI000017378E

A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R:Penstingl, H.; Hilschmann, N.

Ig gamma-2c chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma 4 chain c
Ig gamma heavy cha
Ig epsilon chain C
Ig heavy chain VHI
Ig heavy chain V-1
Ig heavy chain pre
Ig gamma-1 chain C
Ig gamma-1 heavy c
Ig heavy chain (DO

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the GIm(17) and GIm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 Ko
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the GIm(3) and GIm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;109,112/Disulfide bonds: interchain (to light chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 98.0%; Score 1729; DB 1; Length 330;
Best Local Similarity 97.9%; Pred. No. 1.2e-113;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDTHTCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDTHTCPCPAPELLGG 120
Qy 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREPQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREPQYN 180
Qy 181 STYRVSVSLTVLHQNWMNGKEYCKCKSVNKPALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVSVSLTVLHQNWMNGKEYCKCKSVNKPALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Qy 241 LTRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
Db 241 LTRKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
Qy 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

||||| 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
Db
RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM>
Query Match 90.3%; Score 1592.5; DB 2; Length 377;
Best Local Similarity 80.1%; Pred. No. 4.8e-104;
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;
Qy 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQSS 60
Qy 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVKV----- 98
Db 61 GLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKVKELKPTGLDTHTCPCRPBKSC 120
Qy 99 -----EPKCDKTHTCPCPAPELLGSGSVFLFPKPKDT 133
Db 121 DTPPPCPCRPBKSCDTPPPCPCRPBKSCDTPPPCPCPAPELLGSGSVFLFPKPKDT 180
Qy 134 LMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVSVTLVLH 193
Db 181 LMSRTPETVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYNSTYRVSVTLVLH 240
Qy 194 QNMNGKEYCKCKSVNKPALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 253
Db 241 QDWLNGKEYCKCKSVNKPALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVK 300
Qy 254 GFYPDSIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRWQGNVFCSCVMHE 313
Db 301 GFYPDSIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRWQGNVFCSCVMHE 360
Qy 314 ALHNHYQORSLSLSPGK 330
Db 361 ALHNRTQKSLSLSPGK 377
RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an IGHG4 conver
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA

A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:QBN4Y9; UNIPARC:UPI0000176FOB
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>

Query Match 90.2%; Score 1590.5; DB 2; Length 377;
Best Local Similarity 80.1%; Pred. No. 6.6e-104;
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNKTKVKKV----- 98
DB 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNKTKVKKV----- 98
QY 99 -----EPKSCDKHTHTCPAPPELLGGPSVFLFPPPKPKDT 133
DB 121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPAPPELLGGPSVFLFPPPKPKDT 180
QY 134 LMSRTPETCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYNSTYRVSVLTVLH 193
DB 181 LMSRTPETCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYNSTYRVSVLTVLH 240
QY 194 QNMNGKEYCKVSKNALKAPAEKTIKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVK 253
DB 241 QNLNGKEYCKVSKNALKAPAEKTIKAKVOPREPQVYTLPPSRDELTKNOVSLTCLVK 300
QY 254 GFYPDSIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMHE 313
DB 301 GFYPDSIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRWQGNVFSQVMHE 360
QY 314 ALNHYQORSLSPGK 330
DB 361 ALNHYQORSLSPGK 377

RESULT 4

IG gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32
A:Note: Iys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein rll
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', '21-57, 'Z', '59, 'A', '61-193, 'D', '195-325 <MAN>
A:Cross-references: UNIPARC:UPI0000173791
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', '26-57, 'EV', '60-85, '132-171, 'ZZZ', '175, 'B', '177-193, 'D', '195-196, 'Q', '198-
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793

A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.8%; Score 1566; DB 1; Length 326;
Best Local Similarity 89.1%; Pred. No. 2.8e-102;
Matches 294; Conservative 15; Mismatches 17; Indels 4; Gaps 2;

QY 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNKTKVKKVPEKSCDKHTHTCPAPPELLGG 120
DB 61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNKTKVKKVPEKSCDKHTHTCPAPPELLGG 116
QY 121 PSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYN 180
DB 117 PSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREEQYN 176
QY 181 STYRVSVLTVLHQNMMNGKEYCKVSKNALKAPAEKTIKAKVOPREPQVYTLPPSRDE 240
DB 177 STYRVSVLTVLHQNMMNGKEYCKVSKNALKAPAEKTIKAKVOPREPQVYTLPPSRDE 236
QY 241 LTKNOVSLTCLVKGYFSDIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRW 300
DB 237 MTKNQVSLTCLVKGYFSDIAVWESNGQPNENYKTPPVLDSVGSFFLYSKLTVDKSRW 296
QY 301 QGNVFSQVMHEALNHYQORSLSPGK 330
DB 297 QGNVFSQVMHEALNHYQORSLSPGK 326

RESULT 5
G4HU

Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:93157104; PMID:6299662
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A;Note: the sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30,81-326 <PIN>
A;Cross-references: UNIPARC:UPI00000173795; UNIPARC:UPI00000173796
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.0%; Score 1552.5; DB 1; Length 327;
Best Local Similarity 88.8%; Pred. No. 2.5e-101;
Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;

Qy 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 60
Db 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 60

Qy 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPCPAPPELLGG 117

Qy 121 PSVFLPFPKPDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 180
Db 118 PSVFLPFPKPDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 177

Qy 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPVYTLPPSRDE 240
Db 178 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPVYTLPPSRDE 237

Qy 241 LTRKQVSLTCLVKGFPYPSDIAVEVESNGQPENNYKTPPVLDSDGVSFFLYSKLTVDKSRW 300
Db 238 MTKNQVSLTCLVKGFPYPSDIAVEVESNGQPENNYKTPPVLDSDGVSFFLYSKLTVDKSRW 297

Qy 301 QQGNVFCSCNVHEALHNHYTQKSLSLSPGK 330
Db 298 QQGNVFCSCNVHEALHNHYTQKSLSLSPGK 327

RESULT 6
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140,'C',142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 69.5%; Score 1225.5; DB 2; Length 374;
Best Local Similarity 87.1%; Pred. No. 2.2e-78;
Matches 230; Conservative 6; Mismatches 17; Indels 11; Gaps 2;

Qy 78 TOTYICNVN-----HK-PSNTKVDKVPKSCDKTHTCPCPAPPELLGSPVFLF 126
Db 111 TATYCGYVEGVGGYRFSHNGQGLTVTVSSEPKSCDKTHTCPCPAPPELLGSPVFLF 170

Qy 127 PPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYNSTYRVV 186
Db 171 PPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYNSTYRVV 230

Qy 187 SVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPVYTLPPSRDELTKNOV 246
Db 231 SVLTVLHQNWMNGKEYCKVSNKALPAPIETISKAKVQPREPVYTLPPSRDELTKNOV 290

Qy 247 SLTCLVKGFPYPSDIAVEVESNGQPENNYKTPPVLDSDGVSFFLYSKLTVDKSRWQGNVF 306
Db 291 SLTCLVKGFPYPSDIAVEVESNGQPENNYKTPPVLDSDGVSFFLYSKLTVDKSRWQGNVF 350

Qy 307 SCSVMHEALHNHYTQKSLSLSPGK 330
Db 351 SCSVMHEALHNHYTQKSLSLSPGK 374

RESULT 7
I47159
Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47159; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
C;Genetics:
A;Gene: IGG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 69.4%; Score 1225; DB 2; Length 328;
Best Local Similarity 67.5%; Pred. No. 2e-78;
Matches 224; Conservative 46; Mismatches 56; Indels 6; Gaps 2;

Qy 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 60
Db 1 APKTAPSVFLPAPSSKSTSGTAAAGCLVVDVSHEDPEVKFNWYDGVVHNVTKPRERQYN 60

Db 181 PENNYKTTTPVLDSGFFLYSKLTVDKSRWQQGVFSCSVMEALHNHYTQKS 234

RESULT 11

Ig gamma 1 chain constant region - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C/Accession: I47158

R/Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A/Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B

A/Reference number: I47158; MUID:95015845; PMID:7930579

A/Accession: I47158

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-328 <KAC>

A/Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:g433121; PIDN:AAA52216.1; PI

C/Genetics:

A/Gene: IgG1

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F/133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 1193; DB 2; Length 328;

Best Local Similarity 67.2%; Pred. No. 3.4e-76;

Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;

Qy 1 ASTKGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Db 1 AKPTAPSVFLPACGRDVGPNVALGGLASSYFPPEPVTVTWSGALTSGVHTFPAVLQPS 60

Qy 61 GLYSLSVTVTPSSSLGTQYICNVAKPSNTKVDKVEPKSCDKHTCCPCAPPELLGG 120

Db 61 GLYSLSVMVTPASSLSKSYTCNVNHPATTTKVDKRV---GIHQPTCIPCGCE-VAG 116

Qy 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

Db 117 PSVFIFFPKDPTLMISQTEVTCVVVDVSHKEAEVQFSYVDGVEVHTAETRPKEQFN 176

Qy 181 STYRVSVLTVLHQNWMNGKEYCKYKSNKALPAPIETKISKAKVQPREQVYTLPPSRDE 240

Db 177 STYRVSVLPIHQDWLKGKFEKCKVNNVLDLPAPITRTISKAKGSRQPREQVYTLPPAAE 236

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEHESNGQ--PENNYKTTTPVLDSVCSFELYSLKLTVDKS 298

Db 237 LRSKVTLTCLVIGFYPDIHVEWKSNGQPEPENTYRTTPPQDDVDGTFFLYSLKLAVDKA 296

Qy 299 RWQOGVFCVSMHEALHNHYQQRSLSPGK 330

Db 297 RWDHGDVFECAVMEALHNHYTQKSISKTQK 328

RESULT 12

GHRB

Ig gamma chain C region - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004

C/Accession: A91749; A90290; A93928; A90245; A94416; A02161

R/Bernstein, K.E.; Alexander, C.B.; Mage, R.G.

Immunogenetics 18, 387-397, 1983

A/Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplo

A/Reference number: A91749; MUID:84030930; PMID:6313520

A/Accession: A91749

A/Molecule type: mRNA

A/Residues: 1-323 <BER>

A/Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D

A/Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr

R/Pratt, D.M.; Mole, L.E.

Biochem. J. 151, 337-349, 1975

A/Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob

A/Reference number: A90290; MUID:76135469; PMID:1243651

A/Accession: A90290

A/Molecule type: protein

A/Residues: 1-47,'E',49-71,'PV',72-128 <PRA>

A/Cross-references: UNIPARC:UPI00001737AB

R/Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.

Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982

A/Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain

A/Reference number: A93928; MUID:83299917; PMID:6193512

A/Accession: A93928

A/Molecule type: mRNA

A/Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>

A/Cross-references: UNIPARC:UPI000016CS5D; GB:M16426; NID:gl65111; PIDN:AAA31289.1; PID

A/Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark

R/Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.

Biochem. J. 116, 249-259, 1970

A/Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin

A/Reference number: A90245; MUID:70110015; PMID:5461106

A/Accession: A90245

A/Molecule type: protein

A/Residues: 132-143,'E',145-161 <FRU>

A/Cross-references: UNIPARC:UPI00001737AC

R/Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almqvist and Wiksell.

A/Reference number: A94416

A/Accession: A94416

A/Molecule type: protein

A/Residues: 129-131;155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'

A/Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AB

A/Note: this has the e15 allotypic marker, 185-Ala

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-82/Domain: immunoglobulin homology <IM1>

F/130-199/Domain: immunoglobulin homology <IM2>

F/236-303/Domain: immunoglobulin homology <IM3>

F/173/Binding site: carbonylrate (Asn) #status predicted

Query Match 67.6%; Score 1192.5; DB 1; Length 323;

Best Local Similarity 67.9%; Pred. No. 3.7e-76;

Matches 222; Conservative 37; Mismatches 61; Indels 7; Gaps 2;

Qy 4 KGPSVFLPAPSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 63

Db 4 KAPSVPFLPAPCCGDTPSSTVTILGCLVKGLPEPVTVTWSGTLTNGVTFPFSVRSGLY 63

Qy 64 SLSSVTVTPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKHTCCPCAPPELLGSPV 123

Db 64 SLSSVSVTSSS---QPVTNCNVAHPATNTKVDKTVAPSTCSK----PTCPPPELLGSPV 116

Qy 124 FLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTY 183

Db 117 FIFPPPKDPTLMISRTPEVTCVVVDVSDPDPEVQFTWYINNEQVRTARPPLEQQFNSTI 176

Qy 184 RVSVLTVLHQNWMNGKEYCKYKSNKALPAPIETKISKAKVQPREQVYTLPPSRBELTK 243

Db 177 RVSVTLPIHQDWLKGKFEKCKVNNKALPAPIETKISKARGQPLEPKVYTMGPPRELSS 236

Qy 244 NQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPVLDSVGSFFELYSLKLTVDKSRWQOG 303

Db 237 RVSLSCTMNGFYPSDISVEWEKNGKAEDKTTTPAVLDSGDSFYFLNKLSVFTSEWQRG 296

Qy 304 NVFSCSVMEALHNHYQQRSLSPGK 330

Db 297 DVFTCSVMHEALHNHYTQKSISRSPCK 323

RESULT 13

I47161

Ig gamma 3 chain constant region - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C/Accession: I47161

R/Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47161
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Cross-references: UNIPARC:UPI0000115526; EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PI
C;Genetics:
A;Gene: I9G3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IM>

Query Match 67.4%; Score 1189; DB 2; Length 328;
Best Local Similarity 66.9%; Pred. No. 6.5e-76;
Matches 222; Conservative 43; Mismatches 61; Indels 6; Gaps 3;

QY 1 ASTKGSPVPLAPSSKSTSGTAAAGCLVKDYPPEPTVWSNGALTSVHTPPAVLQSS 60
Db 1 APTATSVPLAPCGRDTSGPNVALGLASSYFPEPTVMTWSGALTSVHTPPAVLQSS 60

QY 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKNTKVDKKVPKSCDKTHCTPPCPAPPELLGG 120
Db 61 GLYSLSVMWTVPASSLSKSYTCNVNHPATTKVDKRVGKT---KPPCPICPGCB-VAG 116

QY 121 PSVFLPPPKPKDTLMTLSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKTKPRBEQYN 180
Db 117 PSVFIFPPKPKDTLMTLSQTEPEVTCVVVDVSHEDPEVKFNMYVDGVEVHTAETRPKEQFN 176

QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 177 STYRVSVLPQIQHDMLGKEFKCKVNNVLDLPAPITRTISKATGQSRBPQVYTLPPABE 236

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNKTTPPPVLDVSGSPFLYSLKTVDSK 298
Db 237 LRSKSVTVCLVIGFPPDPDHLVEMKNGQPEPEGNVTRTPPQQDVGDTFLYSLKLVADKA 296

QY 299 RMOQGNVFCVSNVHEALHNHYQOQSLSLSPGK 330
Db 297 RWDHGETFECAVMEALHNHYTQKSISKTQCK 328

RESULT 14
G2GP
Ig gamma-2 chain C region - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151
R;Trischmann, T.M.
submitted to the Atlas, April 1975
A;Reference number: A94553
A;Accession: A94553
A;Molecule type: protein
A;Residues: 1-3 <TRI>
A;Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
R;Birstein, B.K.; Huseain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Residues: 4-68 <BIR>
A;Cross-references: UNIPARC:UPI000017379F
R;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
A;Reference number: A90359; MUID:71058486; PMID:5538616
A;Accession: A90359
A;Molecule type: protein
A;Residues: 69-133;312-329 <TUR>
A;Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A;Reference number: A90384; MUID:75036072; PMID:4429665
A;Accession: A90384
A;Molecule type: protein
A;Residues: 134-226 <TRA>
A;Cross-references: UNIPARC:UPI00001737A2
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
A;Molecule type: protein
A;Residues: 227-311 <TR2>
A;Cross-references: UNIPARC:UPI00001737A3
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Content: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;135-204/Domain: immunoglobulin homology <IM2>
F;241-310/Domain: immunoglobulin homology <IM3>
F;28-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;248-308/Disulfide bonds: #status experimental

Query Match 66.6%; Score 1174.5; DB 1; Length 329;
Best Local Similarity 68.2%; Pred. No. 6.8e-75;
Matches 227; Conservative 31; Mismatches 66; Indels 9; Gaps 4;

QY 1 ASTKGSPVPLAPSSKSTSGTAAAGCLVKDYFPBPVTVSMNSGALTSVHTPPAVLQSS 60
Db 2 ARTTAPSVPLAASCVDITSSGMWTLGCLVKGYFPEPTVKMNSGALTSVHTPPAVLQ-S 60

QY 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKNTKVDKKVPKSCDKTH--TCPPCPAPPELL 118
Db 61 GLYSLSVMWTVPSSSKAT---CNVAHPASSTKVDKTVPEIRTPZBPBCTCPKCPPENL 116

QY 119 GGPVFLPFPKPKDTLMTLSRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKTKPRREQ 178
Db 117 GGPVSVFIFPPKPKDTLMTLSLTPRVTCVVVDVSDPEVQFTWFDNKNKPVGNAETKPRVEQ 176

QY 179 YNSTYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSR 238
Db 177 YNTTFVESVLPQIQHDMLGKEFKCKVNNVLDLPAPITRTISKATGQSRBPQVYTLPPSR 236

QY 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDVSGSFFLYSLKTV 296
Db 237 DELSKSKSVTVCLIIINFFPADIHVEWASNRVPSKEYKNTTPPIEDADGSGFLYSLKTV 296

QY 297 KSRMOQGNVFCVSNVHEALHNHYQOQSLSLSPG 329
Db 297 KSAWDQGTVYTCVNVHEALHNHYTQKATRSRSPG 329

RESULT 15
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-472 <PAR>
A:Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 1163.5; DB 2; Length 472;
Best Local Similarity 65.7%; Pred. No. 6.3e-74;
Matches 218; Conservative 40; Mismatches 71; Indels 3; Gaps 2;

Qy	1	ASTKGPSEVPLAPSSKSTSGTAALGCLVKDYPEPEPTVTSWNSGALTSGVHTTTPAVLQSS	60
Db	142	ASTTPPKVYPLTSCCGDTSSIVTLGCLVSSYMPPEPTVTSWNSGALTSGVHTTTPAVLQSS	201
Qy	61	GLYSLSSVTVTPSSSLGTQYICNVNHPKNTKYDKKVEPKSCDKTHTCPPCPAPPELLGG	120
Db	202	GLYSLSSVTVTPASTSGAQIFICNVVHPASSTKYDKRVEFGCPDCKHC-RCPPPELPGG	260
Qy	121	PSVFLFPPPKPDKTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN	180
Db	261	PSVFIFPPKPKDKTLTIISGTPEVTCVVVDVGGDDPEVQFSWFVDNVEVRTARTKPREEQFN	320
Qy	181	STYRVSVLTIVLHONWNGKEYCKVSKNKAIPAPIEKTISKAKVQPREPQVYTLPPSRDE	240
Db	321	STFRVVSALPIQHODWTGCKEFCCKVNEALPAPIVRIISRTKGQAREPQVYVLAAPPQEE	380
Qy	241	LTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTPPVLDSDVGSFELYSKLTVDKS	298
Db	381	LSKSTLSVTCLVTGFPDYIAVEWQKNGQPESEDKYGTTSQLDADGSYFLYSRLRVDKN	440
Qy	299	RWQGNVFSCSVMHEALHNHYQRRSLSLSPGK	330
Db	441	SWQEGDTYACVMHEALHNHYTQKSISKPPGK	472

Search completed: February 22, 2006, 21:38:16
Job time : 34.6269 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:24 ; Search time 219.43 Seconds
(without alignments)
1061.041 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGFSVFLAPSSKSTSG.....MHEALHNYQORSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1729	98.0	330	1	IGHG1_HUMAN	P01857 homo sapien
2	1729	98.0	465	2	Q6GKX6_HUMAN	Q6GKX6 homo sapien
3	1729	98.0	469	2	Q569F4_HUMAN	Q569F4 homo sapien
4	1729	98.0	469	2	Q727P5_HUMAN	Q727P5 homo sapien
5	1729	98.0	470	2	Q725W1_HUMAN	Q725W1 homo sapien
6	1729	98.0	470	2	Q6PUA4_HUMAN	Q6PUA4 homo sapien
7	1729	98.0	475	2	Q5EFES_HUMAN	Q5EFES homo sapien
8	1729	98.0	475	2	Q6GMW7_HUMAN	Q6GMW7 homo sapien
9	1729	98.0	476	2	Q6GMX1_HUMAN	Q6GMX1 homo sapien
10	1726	97.8	466	2	Q6IN78_HUMAN	Q6IN78 homo sapien
11	1726	97.8	472	2	Q6N089_HUMAN	Q6N089 homo sapien
12	1725	97.8	473	2	Q6P055_HUMAN	Q6P055 homo sapien
13	1725	97.8	475	2	Q6WZQ6_HUMAN	Q6WZQ6 homo sapien
14	1725	97.8	480	2	Q6N094_HUMAN	Q6N094 homo sapien
15	1725	97.8	481	2	Q6N097_HUMAN	Q6N097 homo sapien
16	1725	97.8	482	2	Q72351_HUMAN	Q72351 homo sapien
17	1722	97.6	466	2	Q6N096_HUMAN	Q6N096 homo sapien
18	1720	97.5	348	2	Q6PYX1_HUMAN	Q6PYX1 homo sapien
19	1720	97.5	478	2	Q6P181_HUMAN	Q6P181 homo sapien
20	1720	97.5	480	2	Q6P1F1_HUMAN	Q6P1F1 homo sapien
21	1718	97.4	475	2	Q6N095_HUMAN	Q6N095 homo sapien
22	1718	97.4	544	2	Q6B395_HUMAN	Q6B395 homo sapien
23	1710	96.9	473	2	Q6MZV7_HUMAN	Q6MZV7 homo sapien
24	1650	94.1	475	2	Q5RE17_PONPY	Q5RE17 pongo pygma
25	1592.5	90.3	518	2	Q6N030_HUMAN	Q6N030 homo sapien
26	1592.5	90.3	519	2	Q5EBM2_HUMAN	Q5EBM2 homo sapien
27	1588.5	90.1	521	2	Q8N4Y9_HUMAN	Q8N4Y9 homo sapien
28	1577.5	89.4	509	2	Q8NF17_HUMAN	Q8NF17 homo sapien
29	1566	88.8	326	1	IGHG2_HUMAN	P01859 homo sapien
30	1566	88.8	417	2	Q6N093_HUMAN	Q6N093 homo sapien
31	1561	88.5	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien

32	1552.5	88.0	327	1	IGHG4_HUMAN	P01861 homo sapien
33	1552.5	88.0	473	2	Q8TC63_HUMAN	Q8TC63 homo sapien
34	1552	88.0	470	2	Q68CN4_HUMAN	Q68CN4 homo sapien
35	1551	87.9	464	2	Q6NZU6_HUMAN	Q6NZU6 homo sapien
36	1543.5	87.5	476	2	Q6MZX7_HUMAN	Q6MZX7 homo sapien
37	1486.5	84.3	354	2	Q86TT2_HUMAN	Q86TT2 homo sapien
38	1228.5	69.6	337	2	Q95M34_HORSE	Q95M34 equus caball
39	1226	69.5	679	2	Q96PQ8_HUMAN	Q96PQ8 homo sapien
40	1210.5	68.6	487	2	Q65ZL2_9MURI	Q65ZL2 mus sp. fv/
41	1192.5	67.6	323	1	GC_RABIT	P01870 oryctolagus
42	1174.5	66.6	329	1	IGHG2_CANPO	P01862 cavia porce
43	1128	63.9	290	1	IGHG3_HUMAN	P01860 homo sapien
44	1117.5	63.4	333	1	GC_B_RAT	P20761 rattus norv
45	1117.5	63.4	469	2	Q5M839_RAT	Q5M839 rattus norv

ALIGNMENTS

RESULT 1	IGHG1_HUMAN	STANDARD;	PRT;	330 AA.
ID	IGHG1_HUMAN			
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]__TaxID=9606;			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	PROTEIN SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Fonstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal			
RT	IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic			
RT	peptides of the H-chain, alignment of the tryptic peptides and			
RT	discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			

RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E.; Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RN Biochemistry 9:3188-3196(1970).
RN [7]
RN DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Aeppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the
CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC GIM(3) marker and the GIM (non-1) markers.
CC -1- MISCELLANEOUS: Nie also differs in the amidation states of 35,
CC 116, 198, 269 and 272.
CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00228; AAC82527.1; ALT_INIT; Genomic DNA.
DR PIR; A93433; GHU.
DR PDB; 1AJ7; X-ray; H=1-103.
DR PDB; 1AQK; X-ray; H=1-103.
DR PDB; 1DSB; X-ray; B/H=1-101.
DR PDB; 1DSI; X-ray; H=1-101.
DR PDB; 1D6V; X-ray; H=1-101.
DR PDB; 1DN2; X-ray; A/B=120-326.
DR PDB; 1E4K; X-ray; A/B=106-330.
DR PDB; 1FC1; X-ray; A/B=106-329.
DR PDB; 1FC2; X-ray; D=108-329.
DR PDB; 1FCC; X-ray; A=121-326.
DR PDB; 1H2H; X-ray; H/K=1-330.
DR PDB; 1I72; X-ray; B/D=1-103.
DR PDB; 1IIS; X-ray; A/B=107-330.
DR PDB; 1IIX; X-ray; A/B=107-330.
DR PDB; 1L6X; X-ray; A=120-326.
DR PDB; 1QOX; X-ray; A/B=119-330.
DR PDB; 1T83; X-ray; A/B=107-330.
DR PDB; 2RCS; X-ray; H=1-103.
DR HGNC; HGNC:5525; IGHG1.
DR MIM; 147100; .
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 3.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 2.
DR 3D-structure; Direct protein sequencing; Glycoprotein;
DR Immunoglobulin C region; Immunoglobulin domain.
DR REGION 1 98 CH1.

FT	REGION	99	110
FT	REGION	111	223
FT	REGION	224	330
FT	CARBOHYD	180	180
FT	DISULFID	27	83
FT	DISULFID	103	103
FT	DISULFID	109	109
FT	DISULFID	112	112
FT	DISULFID	144	204
FT	DISULFID	250	308
FT	VARIANT	97	97
FT			
FT	VARIANT	239	239
FT			
FT	VARIANT	241	241
FT			
FT	NON_TER	1	1
FT	STRAND	23	24
FT	STRAND	26	33
FT	STRAND	38	38
FT	STRAND	41	41
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FT	STRAND	165	167
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FT	STRAND	176	177
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FT	STRAND	183	190
FT	HELIIX	193	197
FT	TURN	198	199
FT	STRAND	202	207
FT	TURN	209	210
FT	STRAND	215	219
FT	STRAND	227	227
FT	STRAND	230	234
FT	HELIIX	238	242
FT	STRAND	245	256
FT	STRAND	261	266
FT	TURN	267	268
FT	STRAND	269	270
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FT	TURN	283	284
FT	STRAND	287	296
FT	HELIIX	297	301
FT	TURN	302	303
FT	STRAND	306	311
FT	TURN	313	314
FT	HELIIX	316	318
FT	STRAND	319	324
SQ	SEQUENCE	330 AA;	36106 MW; 3770EBE106C2FA33D CRC64;

Query Match 98.0%; Score 1729; DB 1; Length 330;
Best Local Similarity 97.9%; Pred. No. 6e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

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Db      1  ASTKGSVPFLAPSSKSTGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY      61  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVKKVPKSCDKTHTCPPCPAPPELLGG 120
Db      61  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVKKVPKSCDKTHTCPPCPAPPELLGG 120
QY      121  PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db      121  PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY      181  STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
Db      181  STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
QY      241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db      241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY      301  QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db      301  QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330

RESULT 2
QGQX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

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DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0DFDB1386E CRC64;

Query Match      98.0%; Score 1729; DB 2; Length 465;
Best Local Similarity 97.9%; Pred. No. 9.3e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1  ASTKGSVPFLAPSSKSTGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 136  ASTKGSVPFLAPSSKSTGGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 195
QY 61  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVKKVPKSCDKTHTCPPCPAPPELLGG 120
Db 196  GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKTKVKKVPKSCDKTHTCPPCPAPPELLGG 255
QY 121  PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 256  PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 315
QY 181  STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 240
Db 316  STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLPPSRDE 375
QY 241  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 376  LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 435
QY 301  QGQNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 436  QGQNVFSCSVMEALHNHYQOQSLSLSPGK 465

RESULT 3
Q569F4 HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.

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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC NIH MGC Project;
RG TISSUE=Lymph;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTTTPAVLQSS 60
Db 140 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTTTPAVLQSS 199

Qy 61 GLYSLSVVTVPSLSLTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120
Db 200 GLYSLSVVTVPSLSLTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 259

Qy 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 260 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 319

Qy 181 STYRVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 320 STYRVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 379

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDVGSGFFLYSLKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDVGSGFFLYSLKLTVDKSRW 439

Qy 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
Db 440 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 469

RESULT 4
Q727P5 HUMAN PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan J.S.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -, mRNA.
DR HSSP; P01857; 1HZH.
DR SMR; Q727P5; 20-469.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTTTPAVLQSS 60
Db 140 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTTTPAVLQSS 199

Qy 61 GLYSLSVVTVPSLSLTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120
Db 200 GLYSLSVVTVPSLSLTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 259

Qy 121 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 260 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 319

Qy 181 STYRVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 320 STYRVSVLTVLHQNMNNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 379

Qy 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDVGSGFFLYSLKLTVDKSRW 300
Db 380 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDVGSGFFLYSLKLTVDKSRW 439

Qy 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
Db 440 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 469

RESULT 5
Q725W1 HUMAN PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan J.S.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -; mRNA.
DR HSP; P01857; IZH.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match 98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCPAPPELLGG 120
DB 201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCPAPPELLGG 260
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 320
QY 181 STYRVSVSLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 321 STYRVSVSLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 440
QY 301 QGQNPVSCSMHEALHNNHYQKSLSPGK 330
DB 441 QGQNPVSCSMHEALHNNHYQKSLSPGK 470
RESULT 6
Q6PJA4_HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSP; P01861; IADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;
Query Match 98.0%; Score 1729; DB 2; Length 470;
Best Local Similarity 97.9%; Pred. No. 9.4e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
DB 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 200
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCPAPPELLGG 120
DB 201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSCDKTHTCPPCPAPPELLGG 260
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 320
QY 181 STYRVSVSLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 321 STYRVSVSLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 380
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300
DB 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 440

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Qy 301 OQGNVFCVWHEALHHYQORSLSLSPGK 330
Db 441 OQGNVFCVWHEALHHYQORSLSLSPGK 470

RESULT 7
ID QSEFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gamma1 heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Belliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RL antibody T125.";
DR EMBL; AY894992; AAM82028.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Signal.
FT SIGNAL.
FT CHAIN.
FT CHAIN.
SQ SEQUENCE 475 AA; 52362 MW; 1367D40D0C7D2859 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 475;
Best Local Similarity 97.9%; Pred. No. 9.5e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db 146 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 205

Qy 61 GLYSLSVSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 120
Db 206 GLYSLSVSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 265

Qy 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 266 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325

Qy 181 STYRVSVLTVLHONWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 326 STYRVSVLTVLHONWNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 385

Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDYGSFPLYSKLTVDKSRW 300
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDYGSFPLYSKLTVDKSRW 445

Qy 301 OQGNVFCVWHEALHHYQORSLSLSPGK 330
Db 446 OQGNVFCVWHEALHHYQORSLSLSPGK 475
```

```
RESULT 8
O6GMW7_HUMAN
ID O6GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC O6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -; mRNA.
DR GO; GO:0016021; C-integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 475;
Best Local Similarity 97.9%; Pred. No. 9.5e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
Db 146 ASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 205

Qy 61 GLYSLSVSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 120
Db 206 GLYSLSVSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCPPCPAPPELLGG 265

Qy 121 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 266 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325
```

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QY 181 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 326 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 385
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSKLTVDKSRW 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSKLTVDKSRW 445
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 446 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 475
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
Q6GNX1 HUMAN
ID Q6GNX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GNX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC073773; AAH73773.1; -; mRNA.
DR GO; GO:0016021; C-integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR0031596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;
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Query Match

98.0%; Score 1729; DB 2; Length 476;

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Best Local Similarity 97.9%; Pred. No. 9.6e-119;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPSPVTVSMNSGALTSGVHTFPAVLQSS 60
Db 147 ASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPSPVTVSMNSGALTSGVHTFPAVLQSS 206
QY 61 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVKVEPKSCDKTHHTCPCPAPELGG 120
Db 207 GLYSLSVVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVKVEPKSCDKTHHTCPCPAPELGG 266
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 267 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 326
QY 181 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 240
Db 327 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKTISKAKVQPREQVYTLPPSRDE 386
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSKLTVDKSRW 300
Db 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSKLTVDKSRW 446
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
Db 447 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 476

RESULT 10
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC072419; AAH72419.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
```


DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
 SQ SEQUENCE 466 AA; 50854 MW; 53EB0CBCEDE81076E CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 466;
 Best Local Similarity 97.6%; Pred. No. 1.5e-118;
 Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLPAPSCKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 60
 DB 137 ASTKGPSVFLPAPSCKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 196
 QY 61 GLYSLSSVTVTPSSSLGTTQYICNVNHKPSNTKVDKVEPKSCDKTHCTPCPAPPELLGG 120
 DB 197 GLYSLSSVTVTPSSSLGTTQYICNVNHKPSNTKVDKVEPKSCDKTHCTPCPAPPELLGG 256
 QY 121 PSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 180
 DB 257 PSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 316
 QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 DB 317 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 376
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVSGFSLYSLKLTVDKSRW 300
 DB 377 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVSGFSLYSLKLTVDKSRW 436
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
 DB 437 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 466

RESULT 11
 Q6N089 HUMAN
 ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
 AC Q6N089;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686f15220.
 GN Name=DKFZp686f15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Rectum tumor;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wilmann S.;
 RL Submitted (JAN-2005) to the ENBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAE45781.1; -, mRNA.
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003597; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG.cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 97.8%; Score 1726; DB 2; Length 472;
 Best Local Similarity 97.6%; Pred. No. 1.6e-118;
 Matches 322; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLPAPSCKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 60
 DB 143 ASTKGPSVFLPAPSCKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 202
 QY 61 GLYSLSSVTVTPSSSLGTTQYICNVNHKPSNTKVDKVEPKSCDKTHCTPCPAPPELLGG 120
 DB 203 GLYSLSSVTVTPSSSLGTTQYICNVNHKPSNTKVDKVEPKSCDKTHCTPCPAPPELLGG 262
 QY 121 PSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 180
 DB 263 PSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 322
 QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 DB 323 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 382
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVSGFSLYSLKLTVDKSRW 300
 DB 383 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVSGFSLYSLKLTVDKSRW 442
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
 DB 443 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 472

RESULT 12
 Q6P055 HUMAN
 ID Q6P055 HUMAN PRELIMINARY; PRT; 473 AA.
 AC Q6P055;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueclin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -, mRNA.
DR HSSP; P01861; 1ADQ.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 473;
Best Local Similarity 97.6%; Pred. No. 1.9e-118;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 144 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 203
QY 61 GLYSLSSVTVPSSSIGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCCPCPAPPELLGG 120
DB 204 GLYSLSSVTVPSSSIGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCCPCPAPPELLGG 263
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 264 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 323
QY 181 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 324 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 383
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
DB 384 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 443
QY 301 QQGNVFSCSVHMEALHNHYQOQSLSLSPGK 330
DB 444 QQGNVFSCSVHMEALHNHYQOQSLSLSPGK 473

RESULT 13
Q6MZQ6 HUMAN
ID Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR SNR; Q6MZQ6; 20-475.

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;
Query Match 97.8%; Score 1725; DB 2; Length 475;
Best Local Similarity 97.6%; Pred. No. 1.9e-118;
Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 146 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 205
QY 61 GLYSLSSVTVPSSSIGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCCPCPAPPELLGG 120
DB 206 GLYSLSSVTVPSSSIGTQYICNVNHPKSTNTKVDKVEPKSCDKTHHTCCPCPAPPELLGG 265
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 266 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 325
QY 181 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240
DB 326 STYRVSVSLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 385
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300
DB 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 445
QY 301 QQGNVFSCSVHMEALHNHYQOQSLSLSPGK 330
DB 446 QQGNVFSCSVHMEALHNHYQOQSLSLSPGK 475

RESULT 14
Q6N094 HUMAN
ID Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O01196.
GN Name=DKFZp686O01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 480;
 Best Local Similarity 97.6%; Pred. No. 1.9e-118;
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 151 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 210
 QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELLGG 120
 DB 211 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELLGG 270
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
 DB 271 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 330
 QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 DB 331 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 390
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFPLYSKLTVDKSRW 300
 DB 391 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFPLYSKLTVDKSRW 450
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
 DB 451 QQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 480

RESULT 15
 Q6N097_HUMAN
 ID Q6N097_HUMAN PRELIMINARY; PRT; 481 AA.
 AC Q6N097;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686H20196.
 GN Name=DKFZp686H20196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Esophagus tumor;
 RG The German cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Pobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640619; CAE45773.1; -, mRNA.
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 97.8%; Score 1725; DB 2; Length 481;
 Best Local Similarity 97.6%; Pred. No. 1.9e-118;
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60
 DB 152 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 211
 QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELLGG 120
 DB 212 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHCTCPCPAPELLGG 271
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
 DB 272 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 331
 QY 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
 DB 332 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 391
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFPLYSKLTVDKSRW 300
 DB 392 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFPLYSKLTVDKSRW 451
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
 DB 452 QQGNVFCSCVMHEGLHNHYTKQSLSLSPGK 481

Search completed: February 22, 2006, 21:37:12
 Job time : 222.43 secs

GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: February 22, 2006, 21:57:24 ; Search time 168.705 Seconds
(without alignments)
817.308 Million cell updates/sec
Title: US-10-000-439-2
Perfect score: 1764
Sequence: 1 ASTKGPSVFPPLAPSSKSTSG.....MHEALHNHYQQRSLSPK 330
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pap:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pap:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pap:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pap:*
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1764	100.0	330	3	US-09-847-208-2
2	1764	100.0	330	4	US-10-000-439-2
3	1732	98.2	330	5	US-10-966-673-29
4	1729	98.0	330	3	US-09-995-898A-15
5	1729	98.0	330	3	US-09-892-949-38
6	1729	98.0	330	4	US-10-047-542-20
7	1729	98.0	330	4	US-10-269-805-68
8	1729	98.0	330	4	US-10-310-719-8
9	1729	98.0	330	4	US-10-112-582-1
10	1729	98.0	330	4	US-10-320-231A-81
11	1729	98.0	330	4	US-10-383-902A-6
12	1729	98.0	330	4	US-10-408-901-2
13	1729	98.0	330	4	US-10-420-034A-15
14	1729	98.0	330	4	US-10-257-907-5
15	1729	98.0	330	4	US-10-656-769-2
16	1729	98.0	330	4	US-10-772-531-38
17	1729	98.0	330	4	US-10-479-326-1
18	1729	98.0	330	5	US-10-815-449-8
19	1729	98.0	330	5	US-10-684-957-2
20	1729	98.0	330	5	US-10-886-838-6
21	1729	98.0	330	5	US-10-822-300-3
22	1729	98.0	330	5	US-10-822-300-7
23	1729	98.0	330	5	US-10-687-118-3
24	1729	98.0	330	5	US-10-687-118-7
25	1729	98.0	330	5	US-10-901-735-2
26	1729	98.0	330	5	US-10-698-907-22
27	1729	98.0	330	5	US-10-928-305-7

28	1729	98.0	330	5	US-10-480-109-5	Sequence 5, Appli
29	1729	98.0	330	5	US-10-891-658-2	Sequence 2, Appli
30	1729	98.0	330	5	US-10-867-506-81	Sequence 81, Appl
31	1729	98.0	330	5	US-10-937-596-31	Sequence 31, Appl
32	1729	98.0	330	5	US-10-893-576-45	Sequence 45, Appl
33	1729	98.0	330	5	US-10-868-373-8	Sequence 8, Appli
34	1729	98.0	330	5	US-10-977-369-139	Sequence 139, App
35	1729	98.0	330	5	US-10-901-736-60	Sequence 60, Appl
36	1729	98.0	330	5	US-10-982-555-38	Sequence 38, Appl
37	1729	98.0	330	6	US-11-004-054-1	Sequence 1, Appli
38	1729	98.0	330	6	US-11-026-998-22	Sequence 22, Appl
39	1729	98.0	330	6	US-11-027-309A-22	Sequence 22, Appl
40	1729	98.0	330	6	US-11-090-836-44	Sequence 44, Appl
41	1729	98.0	330	6	US-11-090-846-44	Sequence 44, Appl
42	1729	98.0	330	6	US-11-090-847-44	Sequence 44, Appl
43	1729	98.0	330	6	US-11-102-403-24	Sequence 24, Appl
44	1729	98.0	332	3	US-09-990-586-98	Sequence 98, Appl
45	1729	98.0	332	4	US-10-310-113-167	Sequence 167, App

ALIGNMENTS

RESULT 1
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UG7 002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match	100.0%	Score 1764;	DB 3;	Length 330;
Best Local Similarity	100.0%	Pred. No. 1.3e-128;		
Matches 330;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS	60	
Db	1	ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS	60	
Qy	61	GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG	120	
Db	61	GLYSSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPPELLGG	120	
Qy	121	PSVFLFPPKPKDITLISRTPETVTVVDSVSHEDPEVKENWYVDGVEVHNKTKPREEQYN	180	
Db	121	PSVFLFPPKPKDITLISRTPETVTVVDSVSHEDPEVKENWYVDGVEVHNKTKPREEQYN	180	
Qy	181	STYRVSVVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLTPSRDE	240	
Db	181	STYRVSVVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPVVTLTPSRDE	240	
Qy	241	LTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDVSGVCSFLYSLKTVDKSRW	300	
Db	241	LTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDVSGVCSFLYSLKTVDKSRW	300	
Qy	301	QQGNVFSCSVMHEALHNHYQQRSLSPK 330		
Db	301	QQGNVFSCSVMHEALHNHYQQRSLSPK 330		

RESULT 2

US-10-000-439-2
 ; Sequence 2, Application US/10000439
 ; Publication No. US20030064063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saxon, Andrew
 ; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
 ; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
 ; FILE REFERENCE: UC067.004A
 ; CURRENT APPLICATION NUMBER: US/10/000.439
 ; CURRENT FILING DATE: 2001-10-24
 ; PRIOR APPLICATION NUMBER: US 09/847,208
 ; PRIOR FILING DATE: 2001-05-01
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-000-439-2

Query Match 100.0%; Score 1764; DB 4; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.3e-128;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Qy 61 GLYSLSVVTPVSSSLGTQTYICNVNHPKSNKVKVPEKSCDKTHTCPPCPAPPELLGG 120
 Db 61 GLYSLSVVTPVSSSLGTQTYICNVNHPKSNKVKVPEKSCDKTHTCPPCPAPPELLGG 120
 Qy 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 Db 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 Qy 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Db 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVSGSFLLYSLKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVSGSFLLYSLKLTVDKSRW 300
 Qy 301 QQGNVFSCSVNHEALHNHYQORSLSLSPGK 330
 Db 301 QQGNVFSCSVNHEALHNHYQORSLSLSPGK 330

RESULT 3

US-10-966-673-29
 ; Sequence 29, Application US/10966673
 ; Publication No. US20050226864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Design Labs, Inc.
 ; APPLICANT: Hinton, Paul R
 ; APPLICANT: Tsurushita, Naoya
 ; TITLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
 ; FILE REFERENCE: 05982.0039.NPUS07
 ; CURRENT APPLICATION NUMBER: US/10/966.673
 ; CURRENT FILING DATE: 2004-10-15
 ; PRIOR APPLICATION NUMBER: US 60/562,627
 ; PRIOR FILING DATE: 2004-04-14
 ; PRIOR APPLICATION NUMBER: US 60/511,687
 ; PRIOR FILING DATE: 2003-10-15
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 29
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-10-966-673-29

Query Match 98.2%; Score 1732; DB 5; Length 330;
 Best Local Similarity 98.2%; Pred. No. 4e-126; 4; Indels 0; Gaps 0;
 Matches 324; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Qy 61 GLYSLSVVTPVSSSLGTQTYICNVNHPKSNKVKVPEKSCDKTHTCPPCPAPPELLGG 120
 Db 61 GLYSLSVVTPVSSSLGTQTYICNVNHPKSNKVKVPEKSCDKTHTCPPCPAPPELLGG 120
 Qy 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 Db 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 Qy 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Db 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVSGSFLLYSLKLTVDKSRW 300
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVSGSFLLYSLKLTVDKSRW 300
 Qy 301 QQGNVFSCSVNHEALHNHYQORSLSLSPGK 330
 Db 301 QQGNVFSCSVNHEALHNHYQORSLSLSPGK 330

RESULT 4

US-09-995-898A-15
 ; Sequence 15, Application US/09995898A
 ; Publication No. US20030027253A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Xu, Wenfeng
 ; APPLICANT: No. US20030027253Alak, Julia E.
 ; APPLICANT: Whitmore, Theodore E.
 ; APPLICANT: Grant, Francis J.
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
 ; FILE REFERENCE: 00-108
 ; CURRENT APPLICATION NUMBER: US/09/995,898A
 ; CURRENT FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/253,561
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/267,211
 ; PRIOR FILING DATE: 2001-02-07
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-995-898A-15

Query Match 98.0%; Score 1729; DB 3; Length 330;
 Best Local Similarity 97.9%; Pred. No. 6.8e-126; 4; Indels 0; Gaps 0;
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTFAVLQSS 60
 Qy 61 GLYSLSVVTPVSSSLGTQTYICNVNHPKSNKVKVPEKSCDKTHTCPPCPAPPELLGG 120
 Db 61 GLYSLSVVTPVSSSLGTQTYICNVNHPKSNKVKVPEKSCDKTHTCPPCPAPPELLGG 120
 Qy 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 Db 121 PSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
 Qy 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAGQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 5
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-949-38

Query Match 98.0%; Score 1729; DB 3; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
Db 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKVOPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKVOPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 6
US-10-047-542-20
; Sequence 20, Application US/10047542

; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; .SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-20

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
Db 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPPELLGG 120
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKVOPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKVOPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 7
US-10-269-805-68
; Sequence 68, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
; APPLICANT: OLINER, JONATHAN D.
; TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
; FILE REFERENCE: A-722
; CURRENT APPLICATION NUMBER: US/10/269,805
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/328,604
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 76
; .SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-68

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180
QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 8

US-10-310-719-8
; Sequence 8, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region

US-10-310-719-8

Query Match 98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180
QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 300

Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 9
US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match 98.0%; Score 1729; DB 4; Length 330;

Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREQYN 180
QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYITLPPSRDE 240
Db 181 STYRVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330
RESULT 10
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19

;; PRIOR APPLICATION NUMBER: US 60/342,174
;; PRIOR FILING DATE: 2001-12-17
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 81
;; LENGTH: 330
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-320-231A-81

Query Match 98.0%; Score 1729; DB 4; Length 330;

Best Local Similarity 97.9%; Pred. No. 6.8e-126;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

DB 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 11

US-10-383-902A-6

;; Sequence 6, Application US/10383902A

;; Publication No. US20030224408A1

;; GENERAL INFORMATION:

;; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus

;; APPLICANT: Mullberg, Jurgen

;; APPLICANT: Ladner, Robert C.

;; TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY

;; FILE REFERENCE: 10280-042001

;; CURRENT APPLICATION NUMBER: US/10/383,902A

;; CURRENT FILING DATE: 2003-03-07

;; PRIOR APPLICATION NUMBER: US 60/362,403

;; PRIOR FILING DATE: 2002-03-07

;; NUMBER OF SEQ ID NOS: 58

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 6

;; LENGTH: 330

;; TYPE: PRT

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: synthetically generated plasmid sequence

US-10-383-902A-6

Query Match 98.0%; Score 1729; DB 4; Length 330;

Best Local Similarity 97.9%; Pred. No. 6.8e-126;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

DB 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 12

US-10-408-901-2

;; Sequence 2, Application US/10408901

;; Publication No. US2004002313A1

;; GENERAL INFORMATION:

;; APPLICANT: Boyle, William

;; APPLICANT: Huang, Haichun

;; APPLICANT: Elliott, Robin

;; APPLICANT: Sullivan, John

;; APPLICANT: Medlock, Eugene

;; APPLICANT: Martin, Francis

;; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway

;; FILE REFERENCE: MBH 01-1145-A

;; CURRENT APPLICATION NUMBER: US/10/408,901

;; CURRENT FILING DATE: 2003-04-07

;; NUMBER OF SEQ ID NOS: 76

;; SOFTWARE: PatentIn version 3.0

;; SEQ ID NO 2

;; LENGTH: 330

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-10-408-901-2

Query Match 98.0%; Score 1729; DB 4; Length 330;

Best Local Similarity 97.9%; Pred. No. 6.8e-126;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHHTCCPPCPAPPELLGG 120

QY 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

DB 121 PSVELFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

DB 181 STYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 13


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US-10-420-034A-15
; Sequence 15, Application US/10420034A
; Publication No. US20040029228A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20040029228A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Klucher, Kevin M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; FILE REFERENCE: 02-10
; CURRENT APPLICATION NUMBER: US/10/420,034A
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,813
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-420-034A-15

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVVSVLTVHLQWNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVVSVLTVHLQWNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 15
US-10-656-769-2
; Sequence 2, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Allison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-2

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVVSVLTVHLQWNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVVSVLTVHLQWNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240

US-10-420-034A-15
; Sequence 15, Application US/10420034A
; Publication No. US20040029228A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20040029228A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Klucher, Kevin M.
; TITLE OF INVENTION: CYTOKINE RECEPTOR
; FILE REFERENCE: 02-10
; CURRENT APPLICATION NUMBER: US/10/420,034A
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/373,813
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-420-034A-15

Query Match      98.0%; Score 1729; DB 4; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.8e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVSWNSGALTSGVHTTTPAVLQSS 60
Qy 61 GLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Qy 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Qy 181 STYRVVSVLTVHLQWNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Db 181 STYRVVSVLTVHLQWNLNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSVGSFPLYSKLTVDKSRW 300
Qy 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
Db 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 14
US-10-257-907-5
; Sequence 5, Application US/10257907
; Publication No. US20040043022A1
; GENERAL INFORMATION:
; APPLICANT: Heuer, Josef
; APPLICANT: Liu, Jingqi
; APPLICANT: Na, Songqing
; APPLICANT: Song, Ho Yeong
; APPLICANT: Yang, Derek Di
; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY
; FILE REFERENCE: X-13992
; CURRENT APPLICATION NUMBER: US/10/257,907
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 330
; TYPE: PRT
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Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVGFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGVGFLYSKLTVDKSRW 300

Qy 301 QQGNVFSCSVMEALHNHYQQRSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQQRSLSLSPGK 330

Search completed: February 22, 2006, 22:03:08
Job time : 170.705 secs

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:58:19 ; Search time 17.0984 Seconds
(without alignments)
287.324 Million cell updates/sec

Title: US-10-000-439-2

Perfect score: 1764

Sequence: 1 ASTKGSPVFPPLAPSSKSTSG.....MHEALHNHYQORSLSLSPGK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pap.*
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7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1729	98.0	330	6	US-10-886-383-6
2	1729	98.0	330	6	US-10-493-909-20
3	1729	98.0	330	6	US-10-982-440-68
4	1729	98.0	330	7	US-11-022-289-11
5	1729	98.0	330	7	US-11-075-351-1
6	1729	98.0	330	7	US-11-165-141-15
7	1729	98.0	330	7	US-11-102-621-3
8	1729	98.0	330	7	US-11-102-621-7
9	1729	98.0	330	7	US-11-005-726-164
10	1729	98.0	330	7	US-11-124-620-1
11	1729	98.0	330	7	US-11-233-683-1
12	1729	98.0	335	7	US-11-024-251-35
13	1729	98.0	444	7	US-11-172-320-6
14	1729	98.0	444	7	US-11-173-969-6
15	1729	98.0	450	7	US-11-005-726-161
16	1729	98.0	450	7	US-11-049-536-701
17	1729	98.0	451	7	US-11-158-505-33
18	1729	98.0	470	7	US-11-072-512-3730
19	1729	98.0	551	7	US-11-022-289-7
20	1729	98.0	551	7	US-11-022-289-8
21	1729	98.0	557	7	US-11-022-289-4
22	1729	98.0	557	7	US-11-022-289-5
23	1729	98.0	557	7	US-11-022-289-6
24	1727	97.9	592	7	US-10-016-686-4
25	1726	97.8	330	7	US-11-102-621-71

ALIGNMENTS

RESULT 1

US-10-886-383-6

; Sequence 6, Application US/10886383

; Publication No. US20060005571A1

; GENERAL INFORMATION:

; APPLICANT: Hoffmann-La Roche Inc.

; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use

; TITLE OF INVENTION: thereof

; FILE REFERENCE: 21695

; CURRENT APPLICATION NUMBER: US/10/886,383

; CURRENT FILING DATE: 2004-07-08

; PRIOR APPLICATION NUMBER: EP 03015526

; PRIOR FILING DATE: 2003-07-10

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 6

; LENGTH: 330

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-886-383-6

Query Match 98.0%; Score 1729; DB 6; Length 330;

Best Local Similarity 97.9%; Pred. No. 2.8e-132;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60

Db 1 ASTKGSPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120

Db 61 GLYSLSVVVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120

QY 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

Db 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLVTLVHONMNGKEYCKVSKNALKAPAEKTIISKAKVOPREPQVYVTLPPSRDE 240

Db 181 STYRVSVLVTLVHONMNGKEYCKVSKNALKAPAEKTIISKAKVOPREPQVYVTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300

Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300

QY 301 QGQNVFSCSMHEALHNHYQORSLSLSPGK 330

Db 301 QGQNVFSCSMHEALHNHYQORSLSLSPGK 330

```
; ORGANISM: Homo sapiens
US-10-982-440-68

Query Match      98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCCPCPAPELLGG 120
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCCPCPAPELLGG 120
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 4
US-11-022-289-11
; Sequence 11, Application US/11022289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-11

Query Match      98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCCPCPAPELLGG 120
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCCPCPAPELLGG 120
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300

; ORGANISM: Homo sapiens
US-10-493-909-20
; Sequence 20, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; AC'LICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-20

Query Match      98.0%; Score 1729; DB 6; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTTTPAVLQSS 60
QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCCPCPAPELLGG 120
DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHHTCCPCPAPELLGG 120
QY 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330
DB 301 QQGNVFSCSVNHEALHNHYTQKSLSLSPGK 330

RESULT 3
US-10-982-440-68
; Sequence 68, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
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Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 5

US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; TITLE OF INVENTION: AND METHODS FOR PRODUCING THEM
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 120
Db 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 120
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIETKISKAKQVPPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIETKISKAKQVPPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 6

US-11-165-141-15
; Sequence 15, Application US/11165141
; Publication No. US20050266485A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Novak, Julia E.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/11/165,141
; CURRENT FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US/09/995,898
; PRIOR FILING DATE: 2001-11-28

; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-141-15

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 120
Db 61 GLYSLSSVTVFPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPCPAPELGG 120
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
QY 181 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIETKISKAKQVPPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHQNMMGKEYCKVSNKALPAPIETKISKAKQVPPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 7

US-11-102-621-3
; Sequence 3, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-3

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEESGNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEESGNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
RESULT 8
US-11-102-621-7
; Sequence 7, Application US/11102621
; Publication No. US20050278799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102.621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Humanized antibody
US-11-102-621-7

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEESGNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEESGNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
RESULT 9
US-11-005-726-164
; Sequence 164, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORF, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566
; PRIOR FILING DATE: 2002-11-11
; PRIOR APPLICATION NUMBER: EP 01126858.8
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
; OTHER INFORMATION: constant region
US-11-005-726-164

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCCPCPAPELLGG 120
QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEESGNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEESGNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
Db 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330

RESULT 10
US-11-124-620-1
; Sequence 1, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Bang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur

; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-1

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHHTCPCPAPPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHHTCPCPAPPELLGG 120

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

QY 301 QGQNVFSCSVMEALHNHYQORSLSPGK 330
Db 301 QGQNVFSCSVMEALHNHYQORSLSPGK 330

RESULT 11
US-11-233-683-1
; Sequence 1, Application US/11233683
; Publication No. US20060025573A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/11/233,683
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1

Query Match 98.0%; Score 1729; DB 7; Length 330;
Best Local Similarity 97.9%; Pred. No. 2.8e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHHTCPCPAPPELLGG 120
Db 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHHTCPCPAPPELLGG 120

QY 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
Db 121 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 181 STYRVSVLTVLHONMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

QY 301 QGQNVFSCSVMEALHNHYQORSLSPGK 330
Db 301 QGQNVFSCSVMEALHNHYQORSLSPGK 330

RESULT 12
US-11-024-251-35
; Sequence 35, Application US/11024251
; Publication No. US20050266425A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: IGG Secreted Constant Domain
US-11-024-251-35

Query Match 98.0%; Score 1729; DB 7; Length 335;
Best Local Similarity 97.9%; Pred. No. 2.9e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 6 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 65

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHHTCPCPAPPELLGG 120
Db 66 GLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHHTCPCPAPPELLGG 125

QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
DB 126 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 185
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 186 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 245
QY 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDVSGVGFPLYSKLTVDKSRW 300
DB 246 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDVSGVGFPLYSKLTVDKSRW 305
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
DB 306 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 335

RESULT 13
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US2005024413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6

Query Match 98.0%; Score 1729; DB 7; Length 444;
Best Local Similarity 97.9%; Pred. No. 4e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPAVLQSS 60
DB 115 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPAVLQSS 174
QY 61 GLYSLSVVTVSPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 120
DB 175 GLYSLSVVTVSPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 234
QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
DB 235 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 294
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 295 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 354
QY 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDVSGVGFPLYSKLTVDKSRW 300
DB 355 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDVSGVGFPLYSKLTVDKSRW 414
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
DB 414 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 414

RESULT 15
US-11-005-726-161
; Sequence 161, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566

DB 415 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 444

RESULT 14
US-11-173-969-6
; Sequence 6, Application US/11173969
; Publication No. US20050271672A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/11/173,969
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/150,475
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-11-173-969-6

Query Match 98.0%; Score 1729; DB 7; Length 444;
Best Local Similarity 97.9%; Pred. No. 4e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPAVLQSS 60
DB 115 ASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVMSWGALTSGVHTFPAVLQSS 174
QY 61 GLYSLSVVTVSPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 120
DB 175 GLYSLSVVTVSPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPCPAPELLGG 234
QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
DB 235 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 294
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
DB 295 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 354
QY 241 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDVSGVGFPLYSKLTVDKSRW 300
DB 355 LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDVSGVGFPLYSKLTVDKSRW 414
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330
DB 415 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 444

RESULT 15
US-11-005-726-161
; Sequence 161, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLENDORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566

Thu Feb 23 13:14:53 2006

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; PRIOR FILING DATE: 2002-11-11
; PRIOR APPLICATION NUMBER: EP 01126858.8
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
US-11-005-726-161

Query Match      98.0%; Score 1729; DB 7; Length 450;
Best Local Similarity 97.9%; Pred. No. 4.1e-132;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 ASTKGSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB      121 ASTKGSPVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 180

QY      61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHTCPPCPAPPELLGG 120
DB      181 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKKVPEPKSCDKTHTCPPCPAPPELLGG 240

QY      121 PSVFLFPPPKPDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 180
DB      241 PSVFLFPPPKPDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNVKTKPREEQYN 300

QY      181 STYRVVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB      301 STYRVVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 360

QY      241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFELYSLTVDKSRW 300
DB      361 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDVGSFELYSLTVDKSRW 420

QY      301 QQGNVFSCSWMHEALHNHYQQRSLSLSPGK 330
DB      421 QQGNVFSCSWMHEALHNHYQQRSLSLSPGK 450
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Search completed: February 22, 2006, 22:03:44
Job time : 19.0984 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2006, 21:31:15 ; Search time 23.6408 Seconds
(without alignments)
944.229 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQRRLSLSLSPCK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1225	97.2	370	1 GHU	Ig gamma-1 chain C
2	1219	96.7	334	2 S69339	Ig heavy chain V r
3	1217	96.6	255	4 S31866	Ig gamma-1 chain C
4	1172	93.0	234	2 PT0207	Ig gamma chain C r
5	1138	90.3	377	2 A23511	Ig gamma-3 chain C
6	1136	90.2	377	2 A60764	Ig gamma-3 chain C
7	1123	89.1	289	1 G3HUMI	Ig gamma-3 heavy c
8	1107	87.9	326	1 G2HU	Ig gamma-2 chain C
9	1097	87.1	327	1 G4HU	Ig gamma-4 chain C
10	883	70.1	323	1 GHRB	Ig gamma chain C r
11	868.5	68.9	328	2 I47160	Ig gamma 2a chain
12	868.5	68.9	328	2 I47159	Ig gamma 2a chain
13	865	68.7	327	2 I47162	Ig gamma 2a chain c
14	858	68.1	329	1 G2GP	Ig gamma-2 chain C
15	847.5	67.3	328	2 I47158	Ig gamma 1 chain c
16	840.5	66.7	328	2 I47161	Ig gamma 3 chain c
17	820	65.1	470	2 S22080	Ig heavy chain pre
18	813	64.5	333	3 PS0018	Ig gamma-2b chain C
19	812.5	64.5	329	1 G3MSC	Ig gamma-3 chain C
20	811.5	64.4	308	2 C30554	Ig heavy chain C r
21	811.5	64.4	472	2 S31459	Ig gamma-1 chain -
22	801.5	63.6	398	1 G3MSM	Ig gamma-3 chain C
23	794.5	63.1	444	2 PC4436	monoclonal antibod
24	789.5	62.7	324	1 G1MS	Ig gamma-1 chain C
25	784.5	62.3	326	2 PS0017	Ig gamma-1 chain C
26	784.5	62.3	393	1 G1MSM	Ig gamma-1 chain C
27	776.5	61.6	329	2 S00847	Ig gamma-2c chain
28	776	61.6	330	1 G2MSA	Ig gamma-2a chain
29	776	61.6	469	2 S37483	Ig gamma-2a chain

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034COE; EMBL:Z17370

A>Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,

A>Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,

Biochemistry 9, 3161-3170, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A:Cross-references: UNIPARC:UPI000017378D

A>Note: This sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,

A:Cross-references: UNIPARC:UPI000017378E

A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain
Ig gamma-2 chain C
Ig gamma-2b chain
Ig gamma heavy cha
Ig gamma heavy cha
Ig heavy chain VHI
Ig heavy chain V-I
Ig gamma-1 chain C
Ig Y heavy chain C
Ig heavy chain pre
Ig mu chain C regi
Ig mu chain C regi

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie), Igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Cross-references: UNIPARC:UPI000017378F
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KO; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Cross-references: UNIPARC:UPI0000173790
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: Interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: Interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 97.28; Score 1225; DB 1; Length 330;
Best Local Similarity 97.08; Pred. No. 1.7e-85;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNGKEYKCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNGKEYKCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 232
Db 279 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 330
RESULT 2
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
Query Match 96.7%; Score 1219; DB 2; Length 374;
Best Local Similarity 96.1%; Pred. No. 5.5e-85;
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 143 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 202
Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNGKEYKCKVSNKALPAPIEKT 120
Db 203 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNGKEYKCKVSNKALPAPIEKT 262
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 263 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 322
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 232
Db 323 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 374
RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C;Species: Synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filipula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: UNIPARC:UPI000011F41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PI
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
Query Match 96.6%; Score 1217; DB 4; Length 255;
Best Local Similarity 96.6%; Pred. No. 4.9e-85;
Matches 224; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 24 EPKSCDKTHTCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 83
Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNGKEYKCKVSNKALPAPIEKT 120
Db 84 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWMNGKEYKCKVSNKALPAPIEKT 143
C;Species: Homo sapiens (man)

```
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180
|||||
Db 144 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 203
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORSLSLSPGK 232
|||||
Db 204 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORSLSLSPGK 255
|||||

RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991.
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
A:Cross-references: UNIPARC:UPI0000176F05
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 93.0%; Score 1172; DB 2; Length 234;
Best Local Similarity 95.6%; Pred. No. 1.1e-81;
Matches 215; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
Db 10 EPKSCDTTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 69
|||||
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWANGKEYCKVKSNKALPAPIEKT 120
|||||
Db 70 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 129
|||||
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180
|||||
Db 130 ISKAKQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 189
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORS 225
|||||
Db 190 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQKS 234
|||||

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:g33070; PIDN:CAA272
C:Genetic:
A:Gene: IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.3%; Score 1138; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 7.5e-79;
```

```
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
Db 146 EPKSCDTTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 205
|||||
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWANGKEYCKVKSNKALPAPIEKT 120
|||||
Db 206 KMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 265
|||||
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180
|||||
Db 266 ISKTKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 325
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORSLSLSPGK 232
|||||
Db 326 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORSLSLSPGK 377
|||||

RESULT 6
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conversion
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:O8N4Y9; UNIPARC:UPI0000176F0B
C:Superfamily: immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 1136; DB 2; Length 377;
Best Local Similarity 89.7%; Pred. No. 1.1e-78;
Matches 208; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
|||||
Db 146 EPKSCDTTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 205
|||||
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWANGKEYCKVKSNKALPAPIEKT 120
|||||
Db 206 KMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKT 265
|||||
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 180
|||||
Db 266 ISKTKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTP 325
|||||
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORSLSLSPGK 232
|||||
Db 326 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOORSLSLSPGK 377
|||||

RESULT 7
G3HUW1
Ig gamma-3 heavy chain disease proteins - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999
C:Accession: A90442; A92219; A90198; A93915; A02149
R:Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.
Biochemistry 19, 4304-4308, 1980
A:Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain disease protein
A:Reference number: A90442; MUID:81021548; PMID:6774747
A:Contents: heavy chain disease protein Wis
A:Accession: A90442
A:Molecule type: protein
A:Residues: 1-289 <FRA>
```

A;Cross-references: UNIPARC:UPI0000173797
A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain
A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A;Note: the sequence of residues 42-76 was taken from the reference that follows
R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A;Reference number: A92219; MUID:77118561; PMID:402363
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein w
A;Accession: A92219
A;Molecule type: protein
A;Residues: 12-97 <MIC>
A;Cross-references: UNIPARC:UPI0000173798
A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma
idue segment (12-28)
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter
R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the
A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues
A;Accession: A90198
A;Molecule type: protein
A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>
A;Cross-references: UNIPARC:UPI0000173799
A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the
R;Alexander, A.; Steinmetz, M.; Barricault, D.; Frangione, B.; Franklin, E.C.; Hood, L.;
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion
A;Reference number: A93915; MUID:82247835; PMID:6808505
A;Contents: heavy chain disease protein Omn
A;Accession: A93915
A;Molecule type: mRNA
A;Residues: 12-70, 72-114, 116-135, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157
A;Cross-references: UNIPARC:UPI000017379A; UNIPARC:UPI000017379B; UNIPARC:UPI000017379C;
A;Note: a carboxyl-terminal Lys is removed posttranslationally
A;Note: this sequence may represent an allelic form or another gamma chain subclass
C;Comment: The heavy chain disease protein wis is shown.
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 89.1%; Score 1123; DB 1; Length 289;
Best Local Similarity 88.3%; Pred. No. 7.5e-78;
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKSCDTHTCPPCAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKF 60
Dy 59 EPKSCDTPPCPCPCAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVQF 118
Qy 61 NNYVDGVEHNVKTKPREEQNSYRVVSVLTVLHQNMNGKEYKCKVSKNALPAPIEKT 120
Dy 119 KNYVDGVQVHNNAKTKPREQQNSFRVSVLTVLHQNLWDGKEYKCKVSKNALPAPIEKT 178
Qy 121 ISKAKVQPRPQVVTLPSPRDELTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Dy 179 ISKTKGQPRPQVVTLPSPREMTKNQVSLTCLVKGFYPSDIAVEWESSQPENNYNTTP 238
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYQQRSLSLSPG 231
Dy 239 PMLDSGGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFQKSLSLSPG 289

RESULT 8
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:93;
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and i
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein TII
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A;Cross-references: UNIPARC:UPI0000173791
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
A;Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin .
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
A;Cross-references: UNIPARC:UPI0000173794
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83, 140-200, 246-304/Disulfide bonds; #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.9%; Score 1107; DB 1; Length 326;

Best Local Similarity 88.4%; Pred. No. 1.4e-76;
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 ERKCCVE---CPCPAPP--VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 154
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKT 120
DB 155 NMYVDGVEVHNKTKPREEQNFSTFRVSVLTIVHQLNGKEYKCKVSNKGLPAPIEKT 214
QY 121 ISKAKVQPREPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVEWESNGQPNYKTPP 180
DB 215 ISKTKGQPREPQVYTLPPSREENTKQVSLTCLVKGFPSPDIAVEWESNGQPNYKTPP 274
QY 181 PVLDSVGSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 275 PMLDSGDSFPLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 326

RESULT 9
GAHU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299862
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A>Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30; 81-326 <PIN>
A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMI>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/disulfide bonds: interchange (to light chain) #status experimental
F:27-83, 141-201, 247-305/disulfide bonds: #status predicted
F:106, 109/disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.1%; Score 1097; DB 1; Length 327;
Best Local Similarity 90.5%; Pred. No. 8.1e-76;
Matches 201; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

QY 11 CPCCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 70
DB 106 CPSCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 165
QY 71 NVKTKPREEQYNSTYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPRE 130
DB 166 NAKTKPREEQNFSTYRVSVLTVLHQNMMNGKEYKCKVSNKGLFSSIEKTISKAKVQPRE 225

QY 131 PQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVEWESNGQPNYKTPPVLDSVGSFF 190
DB 226 PQVYTLPPSQBEMTKQVSLTCLVKGFPSPDIAVEWESNGQPNYKTPPVLDSVGSFF 285
QY 191 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232
DB 286 LYSRLTVDKSRWQGNVFCSCVMHEALHNNHYQORSLSLSPGK 327

RESULT 10
CHRB
Ig gamma chain C region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 24-Apr-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
R:Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A:Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplo.
A:Reference number: A91749; MUID:84030930; PMID:6313520
A:Accession: A91749
A:Molecule type: mRNA
A:Residues: 1-323 <BER>
A:Cross-references: UNIPROT:P01870; UNIPARC:UPI000012B37D
A>Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Th.
R:Pratt, D.M.; Mole, L.E.
Biochem. J. 151, 337-349, 1975
A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob
A:Reference number: A90290; MUID:76135469; PMID:1243651
A:Accession: A90290
A:Molecule type: protein
A:Residues: 1-47, 'B', 49-71, 'PV', 72-128 <PRA>
A:Cross-references: UNIPARC:UPI00001737AB
R:Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A:Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A:Reference number: A93928; MUID:83299917; PMID:6193512
A:Accession: A93928
A:Molecule type: mRNA
A:Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A:Cross-references: UNIPARC:UPI000016C5ED; GB:M16426; NID:G165111; PIDN:AAA31289.1; PID
R:Richter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
A:Reference number: A90245; MUID:70110015; PMID:5461106
A:Accession: A90245
A:Molecule type: protein
A:Residues: 132-143, 'E', 145-161 <FRU>
A:Cross-references: UNIPARC:UPI00001737AC
R:Hall, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almquist and Wiksell,
A:Reference number: A94416
A:Accession: A94416
A:Molecule type: protein
A:Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', 'C'
A:Cross-references: UNIPARC:UPI00001737AD; UNIPARC:UPI00001737AE
A>Note: this has the e15 allotypic marker, 185-Ala
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-82/Domain: immunoglobulin homology <IM1>
F:130-199/Domain: immunoglobulin homology <IM2>
F:236-303/Domain: immunoglobulin homology <IM3>
F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.1%; Score 883; DB 1; Length 323;
Best Local Similarity 64.5%; Pred. No. 1.3e-59;
Matches 160; Conservative 34; Mismatches 38; Indels 16; Gaps 2;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 44
DB 76 PQVTCNVAPHAATNTKVDKTVAPSTCSTKPTCPPELLGGPSVFIFFPKPKDTLMISRTPEV 135

Qy 45 TCVVVDVSHEDPEVKFNNYV DGEVHN VTKPREEQYNSTYRVVSVLTVLHQWNMNGKEY 104
Db 136 TCVVVDVSDDDPEVQFVTTINNEQVNTARPELPLEQQFNSTIRVIVSTLPIQHDLWLRGKEF 195
Qy 105 KCKVSNKALPAPIEKTISKAKVQPREPVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV 164
Db 196 KCKVHNKALPAPIEKTISKAKGQPLEPKVYTMGPPEELSRSSVSLTCMNGYFPDSIV 255
Qy 165 EWESNGQPENNYKTTPPVLDSDGVFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQR 224
Db 256 EWEKNGKAEDNYKTTPPAVLDSGYSFLYKLSVPTSEWQRGDFVTCVMSVHEALHNNHYTK 315
Qy 225 SLSLSPGK 232
Db 316 SIRSPPGK 323

RESULT 11

I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115525; EMBL:U03780; NID:G433125; PIDN:AAA52218.1; P
C:Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.6e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;
Qy 11 CPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH 70
Db 106 CPICPACE-SPGSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFSWYVDGEVH 164
Qy 71 NVTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKEEQFNSTYRVVSVLPIQHDLWLRGKEFKCKVNNKDLPAPIRIISKAKGQTR 224
Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTPPVLDVSGS 188
Db 225 PQVYTLPPHABELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPPQQVDYGT 284
Qy 189 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNNHYTKSISKTGK 328

RESULT 12

I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>

A:Cross-references: UNIPARC:UPI0000115524; EMBL:U03779; NID:G433123; PIDN:AAA52217.1; P
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 868.5; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 1.6e-58;
Matches 157; Conservative 32; Mismatches 32; Indels 3; Gaps 2;

Qy 11 CPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGEVH 70
Db 106 CPICPACE-SPGSVFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFSWYVDGEVH 164
Qy 71 NVTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKTISKAKVQPRE 130
Db 165 TAQTRPKEEQFNSTYRVVSVLPIQHDLWLRGKEFKCKVNNKDLPAPIRIISKAKGQTR 224
Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTPPVLDVSGS 188
Db 225 PQVYTLPPHABELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTPPQQVDYGT 284
Qy 189 FFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232
Db 285 YFLYSKFSVDKASWQGGGIFQCAVMHEALHNNHYTKSISKTGK 328

RESULT 13

I47162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: UNIPARC:UPI0000115527; EMBL:U03782; NID:G433129; PIDN:AAA52220.1; P
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:82-151/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 865; DB 2; Length 277;
Best Local Similarity 69.0%; Pred. No. 2.5e-58;
Matches 158; Conservative 32; Mismatches 35; Indels 4; Gaps 3;

Qy 8 THTCPPCP-APELLG-GPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 65
Db 49 TKTTPCPICPACGEGPGSAFIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFSWYVD 108
Qy 66 GVEVHNVTKPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKTISKAK 125
Db 109 GVEVHTAQTRPKEEQFNSTYRVVSVLPIQHDLWLRGKEFKCKVNNKDLPAPIRIISKAK 168
Qy 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQ--PENNYKTTPPV 183
Db 169 GQTRPQVYTLPPPTTEELSRKSVITCLVIGFYPPDIDVEWQRNGQPEPEGNRYRTTP 228
Qy 184 DSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSPGK 232
Db 229 DVDGTLYFLYSKLAVDKASWQGGDTFQCAVMHEALHNNHYTKSIFKTPGK 277

RESULT 14

G2GP
Ig gamma-2 chain C region - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004

C:Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein
A:Residues: 1-3 <TRI>
A:Cross-references: UNIPROT:P01862; UNIPARC:UPI000017379E
R:Birshstein, B.K.; Hussein, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
Biochemistry 10, 18-25, 1971
A:Reference number: A90352; MUID:71058471; PMID:5538606
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BIR>
A:Cross-references: UNIPARC:UPI000017379F
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
Biochemistry 10, 9-17, 1971
A:Reference number: A90359; MUID:71058486; PMID:5538616
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133;312-329 <TUR>
A:Cross-references: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90384; MUID:75036072; PMID:4429665
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
A:Reference number: A90385; MUID:75036073; PMID:4609467
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
A:Cross-references: UNIPARC:UPI00001737A3
R:Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
A:Reference number: A90354; MUID:71058474; PMID:4922544
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: immunoglobulin homology <IM1>
F:135-204/Domain: immunoglobulin homology <IM2>
F:241-310/Domain: immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match 68.1%; Score 858; DB 1; Length 329;
Best Local Similarity 67.4%; Pred. No. 1e-57;
Matches 157; Conservative 28; Mismatches 42; Indels 6; Gaps 2;

QY 1 EPKSCDKTTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 101 ZPBPCC----TCPKCPPENLGGPSVFIFFPKPKDTLMISLTPTVTCVVVDVSDQPEVQF 156
QY 61 NWYDGVGVHNVKTPREQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKT 120
DB 157 TWFVDNKPVGNAETKRPVQYNTTFRVESVLPFIHQDNLRGKFKCKVYNKALPAPIEKT 216
QY 121 ISKAKVQRPQVYTLPPSRDELTKNQSLTCLVKGFPSPDI AVEVESNGQP--ENNYKT 178

DB 217 ISKTKGAPRPMDVYTLPPSRDELTKNQSVTLTIINFPFADIHVEWASNRVPVSEKEYKN 276
QY 179 TTPVLDVSGSRFLYSLKLTVDKSRWQGNVFCSSVMHEALHNHYQORSLSLSPG 231
DB 277 TPPIEDADGSGFLYSLKLTVDKSAWDQGTYYTCSVMHEALHNHYTKAISRSPG 329

RESULT 15
I47158
Ig gamma 1 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 21-Jan-2000
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47158
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: UNIPARC:UPI0000115523; EMBL:U03778; NID:G4333121; PIDN:AAA52216.1; P
C:Genetics:
A:Gene: IgG1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 847.5; DB 2; Length 328;
Best Local Similarity 69.3%; Pred. No. 6.4e-57;
Matches 156; Conservative 30; Mismatches 36; Indels 3; Gaps 2;

QY 10 TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 69
DB 105 TCIPICPGCE-VAGPSVFIFFPKPKDTLMISQTPETVCVVVDVSKHAEVQFSWYVDGVEV 163
QY 70 HNVKTPREQYNSTYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPR 129
DB 164 HTAETRPKEEQFNSTYRVSVVLPFIHQDNLGKFKCKVNNVDLPAPITRTTISKATGQSR 223
QY 130 EQVYTLPPSRDELTKNQSLTCLVKGFPSPDI AVEVESNGQ--PENNYKTPPVLDVSG 187
DB 224 EQVYTLPPPAEELSRSKVTTLCLVIGFYPPDIHVEWKSNGQPEPENTYRTTTPPQDDVDG 283
QY 188 SFFLYSLKLTVDKSRWQGNVFCSSVMHEALHNHYQORSLSLSPG 232
DB 284 TFFLYSLKLVADYKARDWDGDKFECAVMHEALHNHYTKSISKTQK 328

Search completed: February 22, 2006, 21:38:17
Job time : 24.6408 secs

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:37:34 ; Search time 34.4594 Seconds
(without alignments)
556.619 Million cell updates/sec

Title: US-10-000-439-3
Perfect score: 1260
Sequence: 1 EPKSCDKTHTCPPCPAPBL.....MHEALHNYQORSLSPGK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/aaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/aaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/aaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/aaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/aaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	1 US-08-595-043A-50	Sequence 50, Appl
2	1225	97.2	232	2 US-09-968-362A-26	Sequence 26, Appl
3	1225	97.2	232	2 US-09-932-812A-26	Sequence 26, Appl
4	1225	97.2	331	2 US-09-178-869-2	Sequence 2, Appl
5	1225	97.2	331	2 US-09-761-413-2	Sequence 2, Appl
6	1225	97.2	360	2 US-09-180-100-11	Sequence 11, Appl
7	1225	97.2	360	2 US-09-949-713-11	Sequence 11, Appl
8	1225	97.2	371	1 US-08-236-311-7	Sequence 7, Appl
9	1225	97.2	371	2 US-08-457-918-7	Sequence 7, Appl
10	1225	97.2	371	2 US-10-157-408-7	Sequence 7, Appl
11	1225	97.2	376	2 US-09-180-100-22	Sequence 22, Appl
12	1225	97.2	376	2 US-09-949-713-22	Sequence 22, Appl
13	1225	97.2	379	2 US-10-679-999-9	Sequence 9, Appl
14	1225	97.2	396	1 US-08-784-512-3	Sequence 3, Appl
15	1225	97.2	396	2 US-09-176-228-3	Sequence 3, Appl
16	1225	97.2	424	4 PCT-US95-03866-12	Sequence 12, Appl
17	1225	97.2	424	4 PCT-US95-03866-14	Sequence 14, Appl
18	1225	97.2	437	4 PCT-US96-10043-11	Sequence 11, Appl
19	1225	97.2	442	4 PCT-US96-10043-9	Sequence 9, Appl
20	1225	97.2	442	4 PCT-US96-10043-7	Sequence 7, Appl
21	1225	97.2	446	1 US-08-397-411-7	Sequence 13, Appl
22	1225	97.2	449	1 US-08-458-516-13	Sequence 16, Appl
23	1225	97.2	452	2 US-09-773-877B-16	Sequence 7, Appl
24	1225	97.2	459	1 US-08-157-101A-7	Sequence 18, Appl
25	1225	97.2	462	2 US-09-773-877B-18	Sequence 41, Appl
26	1225	97.2	467	2 US-08-030-175-41	Sequence 42, Appl
27	1225	97.2	467	2 US-08-030-175-42	Sequence 42, Appl

28	1225	97.2	470	2 US-10-104-047-3730	Sequence 3730, Ap
29	1225	97.2	475	2 US-09-740-002-27	Sequence 27, Appl
30	1225	97.2	476	1 US-08-378-939-10	Sequence 10, Appl
31	1225	97.2	476	2 US-08-487-550-4	Sequence 4, Appl
32	1225	97.2	476	2 US-08-487-550-12	Sequence 12, Appl
33	1225	97.2	476	2 US-09-526-098-4	Sequence 4, Appl
34	1225	97.2	476	2 US-09-526-098-12	Sequence 12, Appl
35	1225	97.2	476	2 US-09-383-916-4	Sequence 4, Appl
36	1225	97.2	476	2 US-09-383-916-12	Sequence 12, Appl
37	1225	97.2	476	2 US-09-758-173-4	Sequence 4, Appl
38	1225	97.2	476	2 US-09-758-173-12	Sequence 12, Appl
39	1225	97.2	476	2 US-09-576-424-4	Sequence 4, Appl
40	1225	97.2	476	2 US-09-576-424-12	Sequence 12, Appl
41	1225	97.2	478	2 US-08-487-550-8	Sequence 8, Appl
42	1225	97.2	478	2 US-09-526-098-8	Sequence 8, Appl
43	1225	97.2	478	2 US-09-383-916-8	Sequence 8, Appl
44	1225	97.2	478	2 US-09-758-173-8	Sequence 8, Appl
45	1225	97.2	478	2 US-09-576-424-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-595-043A-50
; Sequence 50, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-043A-50

Query Match		97.2%	Score 1225;	DB 1;	Length 232;
Best Local Similarity		97.0%	Pred. No. 3.5e-116;		
Matches 225;		Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1	EPKSCDKTHTCPPCPAPBLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
Db	1	EPKSCDKTHTCPPCPAPBLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60		
QY	61	NWYDGVGVHVNKTPREEQNSTYRVVSVLTVLHQNMGNGKEYKCKVSNKALPAPIET	120		
Db	61	NWYDGVGVHVNKTPREEQNSTYRVVSVLTVLHQNMGNGKEYKCKVSNKALPAPIET	120		

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Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232

RESULT 2
US-09-968-362A-26
; Sequence 26, Application US/09968362A
; Patent No. 6797493
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/09/968,362A
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-968-362A-26

Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116; Mismatches 4; Indels 0; Gaps 0;
Matches 225; Conservative 3;

Qy 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232

RESULT 3
US-09-932-812A-26
; Sequence 26, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-932-812A-26

Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232

RESULT 3
US-09-932-812A-26
; Sequence 26, Application US/09932812A
; Patent No. 6900292
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
; TITLE OF INVENTION: increased biological
; TITLE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001
; CURRENT APPLICATION NUMBER: US/09/932,812A
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-09-932-812A-26
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Query Match 97.2%; Score 1225; DB 2; Length 232;
Best Local Similarity 97.0%; Pred. No. 3.5e-116; Mismatches 4; Indels 0; Gaps 0;
Matches 225; Conservative 3;

Qy 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
Db 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232

RESULT 4
US-09-178-869-2
; Sequence 2, Application US/09178869B
; Patent No. 6197294
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
; APPLICANT: Hamang, Joseph P
; APPLICANT: Baetge, E. Edward
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
; FILE REFERENCE: 17810-043
; CURRENT APPLICATION NUMBER: US/09/178,869B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-869-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116; Mismatches 4; Indels 0; Gaps 0;
Matches 225; Conservative 3;

Qy 1 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 100 EPKSCDKHTHTCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 160 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 219
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 220 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
Db 280 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 331

RESULT 5
US-09-761-413-2
; Sequence 2, Application US/09761413
; Patent No. 6506891
; GENERAL INFORMATION:
; APPLICANT: Tao, Weng
; APPLICANT: Wong, Shou
; APPLICANT: Hickey, William F
```

APPLICANT: Hamhang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-761-413-2

Query Match 97.2%; Score 1225; DB 2; Length 331;
Best Local Similarity 97.0%; Pred. No. 5.9e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPALLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 100 EPKSCDKTHTCPPCPAPALLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
QY 61 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
DB 160 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 219
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 220 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 279
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 280 PVLDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 331

RESULT 6
US-09-180-100-11
Sequence 11, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 630639510
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-11

Query Match 97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPALLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 129 EPKSCDKTHTCPPCPAPALLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
QY 61 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
DB 189 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 248
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 309 PVLDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360
RESULT 7
US-09-949-713-11
Sequence 11, Application US/09949713
Patent No. 6953847
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 695384710
APPLICANT: NAGATA, Shigekazu
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/949,713
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/180,100
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/JP97/01502
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-09-949-713-11

Query Match 97.2%; Score 1225; DB 2; Length 360;
Best Local Similarity 97.0%; Pred. No. 6.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCPPCPAPALLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 129 EPKSCDKTHTCPPCPAPALLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188
QY 61 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
DB 189 NNYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 248
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 249 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 308
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
DB 309 PVLDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 360

RESULT 8
US-08-236-311-7
Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311

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; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Haseak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444PIC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9861
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-236-311-7

Query Match          97.2%; Score 1225; DB 1; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116; Indels 0; Gaps 0;
Matches 225; Conservative 3; Mismatches 4;

Qy 1 EPKSCDKHTCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKHTCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 199
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKT 259
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTP 180
Db 260 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTP 319
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 320 PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371

RESULT 9
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918

; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Haseak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444PIC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9861
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-236-311-7

Query Match          97.2%; Score 1225; DB 2; Length 371;
Best Local Similarity 97.0%; Pred. No. 6.9e-116; Indels 0; Gaps 0;
Matches 225; Conservative 3; Mismatches 4;

Qy 1 EPKSCDKHTCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 140 EPKSCDKHTCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 199
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYKCKVSNKALPAPIEKT 120
Db 200 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKALPAPIEKT 259
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTP 180
Db 260 ISKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESNGQPENNYKTP 319
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 320 PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371

RESULT 10
US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
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/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/10/157,408
/   FILING DATE: 28-May-2002
/   CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/   APPLICATION NUMBER: US/08/457,918
/   FILING DATE: 1-JUN-1995
/   APPLICATION NUMBER: 08/236311
/   FILING DATE: 02-MAY-1994
/   APPLICATION NUMBER: 07/936190
/   FILING DATE: 26-AUG-1992
/   APPLICATION NUMBER: 07/842777
/   FILING DATE: 18-FEB-1992
/   APPLICATION NUMBER: 07/250785
/   FILING DATE: 28-SEP-1988
/   APPLICATION NUMBER: 07/104329
/   FILING DATE: 02-OCT-1987
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Kubinec, Jeffrey S.
/   REGISTRATION NUMBER: 36,575
/   REFERENCE/DOCKET NUMBER: P0444PIC3
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 415/225-8228
/   TELEFAX: 415/952-9881
/   INFORMATION FOR SEQ ID NO: 7:
/     SEQUENCE CHARACTERISTICS:
/       LENGTH: 371 amino acids
/       TYPE: amino acid
/       TOPOLOGY: linear
/     SEQUENCE DESCRIPTION: SEQ ID NO: 7:
/
/ US-10-157-408-7
/
/ Query Match          97.2%; Score 1225; DB 2; Length 371;
/ Best Local Similarity 97.0%; Pred. No. 6.9e-116;
/ Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
/
/ QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
/ Db 140 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199
/
/ QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
/ Db 200 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259
/
/ QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
/ Db 260 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 319
/
/ QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
/ Db 320 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 371
/
/ RESULT 11
/ US-09-180-100-22
/ ; Sequence 22, Application US/09180100
/ ; Patent No. 6306395
/ ; GENERAL INFORMATION:
/ ; APPLICANT: NAKAMURA, No. 630639510
/ ; APPLICANT: NAKAMURA, Shigekazu
/ ; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
/ ; FILE REFERENCE: 1110-207P
/ ; CURRENT APPLICATION NUMBER: US/09/180,100
/ ; PRIOR FILING DATE: 1998-11-02
/ ; EARLIER APPLICATION NUMBER: PCT/JP97/01502
/ ; NUMBER OF SEQ ID NOS: 25
/ ; SOFTWARE: PatentIn Ver. 2.0
/ ; SEQ ID NO 22
/ ; LENGTH: 376
/ ; TYPE: PRT
/ ; ORGANISM: Homo sapiens
/
/ US-09-949-713-22
/
/ Query Match          97.2%; Score 1225; DB 2; Length 376;
/ Best Local Similarity 97.0%; Pred. No. 7.1e-116;
/ Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
/
/ QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
/ Db 145 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204
/
/ QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
/ Db 205 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264
/
/ QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
/ Db 265 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 324
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/ QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
/ Db 325 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 376
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/ RESULT 13
/ US-10-679-999-9
/ ; Sequence 9, Application US/10679999
/ ; Patent No. 6936439
/ ; GENERAL INFORMATION:
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/ ORGANISM: Homo sapiens
/ US-09-180-100-22
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/ Query Match          97.2%; Score 1225; DB 2; Length 376;
/ Best Local Similarity 97.0%; Pred. No. 7.1e-116;
/ Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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/ QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
/ Db 145 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204
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/ QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
/ Db 205 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264
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/ QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
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/ QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
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/ RESULT 12
/ US-09-949-713-22
/ ; Sequence 22, Application US/09949713
/ ; Patent No. 6953847
/ ; GENERAL INFORMATION:
/ ; APPLICANT: NAKAMURA, No. 695384710
/ ; APPLICANT: NAGATA, Shigekazu
/ ; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
/ ; FILE REFERENCE: 1110-207P
/ ; CURRENT APPLICATION NUMBER: US/09/949,713
/ ; CURRENT FILING DATE: 2001-09-12
/ ; PRIOR APPLICATION NUMBER: US/09/180,100
/ ; PRIOR FILING DATE: 1998-11-02
/ ; PRIOR APPLICATION NUMBER: PCT/JP97/01502
/ ; PRIOR FILING DATE: 1997-05-01
/ ; NUMBER OF SEQ ID NOS: 25
/ ; SOFTWARE: PatentIn Ver. 2.0
/ ; SEQ ID NO 22
/ ; LENGTH: 376
/ ; TYPE: PRT
/ ; ORGANISM: Homo sapiens
/
/ US-09-949-713-22
/
/ Query Match          97.2%; Score 1225; DB 2; Length 376;
/ Best Local Similarity 97.0%; Pred. No. 7.1e-116;
/ Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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/ QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
/ Db 145 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 204
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/ QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
/ Db 205 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264
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/ QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
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/ QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 232
/ Db 325 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 376
/
/ RESULT 13
/ US-10-679-999-9
/ ; Sequence 9, Application US/10679999
/ ; Patent No. 6936439
/ ; GENERAL INFORMATION:
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; APPLICANT: Mann, Michael B.
; APPLICANT: Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1
; OTHER INFORMATION: /note= "Met (ATG) starts at -1"
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-679-999-9

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Query Match 97.2%; Score 1225; DB 2; Length 379;
Best Local Similarity 97.0%; Pred. No. 7.1e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 2 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 61
Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
Db 62 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIEKT 121
Qy 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 122 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 181
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 232
Db 182 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 233

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RESULT 14
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; Sequence 3, Application US/08784512
; Patent No. 5872209
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETTNER, Frank

```

```

; APPLICANT: CATERSON, Bruce
; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
; TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
; TITLE OF INVENTION: "Aggrecanase" in cell culture systems
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,512
; FILING DATE: 17-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96100682.2
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 18748/311
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..396
; US-08-784-512-3

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Best Local Similarity 97.0%; Pred. No. 7.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Db 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 224
Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
Db 225 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIEKT 284
Qy 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 285 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 344
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 232
Db 345 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 396

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RESULT 15
US-09-176-228-3
; Sequence 3, Application US/09176228
; Patent No. 6180334
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BUETTNER, Frank
; APPLICANT: CATERSON, Bruce

```


APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggregran to study the proteolytic activity of
TITLE OF INVENTION: "Aggregranase" in cell culture systems
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/176,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/784,512
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: EP 96100682.2
FILING DATE: 18-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/311
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..396
US-09-176-228-3

Query Match 97.2%; Score 1225; DB 2; Length 396;
Best Local Similarity 97.0%; Pred. No. 7.6e-116;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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DB 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 224
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQVWNGKEYCKVSNKALPAPIEKT 120
DB 225 NMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQVWNGKEYCKVSNKALPAPIEKT 284
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 285 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 344
QY 181 PVLDSVGSFFLYSKLTVDKSRQQQGNVFCSVNHEALHNHYQOQSLSLSPGK 232
DB 345 PVLDSVGSFFLYSKLTVDKSRQQQGNVFCSVNHEALHNHYQOQSLSLSPGK 396

Search completed: February 22, 2006, 21:39:49
Job time : 35.4594 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2006, 21:57:24 ; Search time 118.604 Seconds
(without alignments)
817.308 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:
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2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1260	100.0	232	3	US-09-847-208-3
2	1260	100.0	232	4	US-10-000-439-3
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4	1260	100.0	330	4	US-10-000-439-2
5	1260	100.0	569	3	US-09-847-208-7
6	1260	100.0	569	4	US-10-000-439-7
7	1228	97.5	330	5	US-10-966-673-29
8	1225	97.2	232	3	US-09-996-357-10
9	1225	97.2	232	3	US-09-389-782-1
10	1225	97.2	232	4	US-10-617-619-7
11	1225	97.2	232	4	US-10-761-593A-26
12	1225	97.2	232	5	US-10-831-622-97
13	1225	97.2	232	5	US-10-800-497-26
14	1225	97.2	232	5	US-10-800-449-26
15	1225	97.2	232	5	US-10-964-215-97
16	1225	97.2	232	6	US-11-016-518A-26
17	1225	97.2	232	6	US-11-017-185-26
18	1225	97.2	234	5	US-10-627-556-684
19	1225	97.2	235	4	US-10-207-655-208
20	1225	97.2	235	5	US-10-627-556-2
21	1225	97.2	235	5	US-10-734-661A-6
22	1225	97.2	247	3	US-09-996-357-13
23	1225	97.2	251	4	US-10-008-063-18
24	1225	97.2	251	4	US-10-152-363A-6
25	1225	97.2	267	3	US-09-996-357-12
26	1225	97.2	269	5	US-10-609-783B-50
27	1225	97.2	285	6	US-11-018-102-11

28	1225	97.2	288	3	US-09-822-851B-14	Sequence 14, Appl
29	1225	97.2	288	4	US-10-119-637A-14	Sequence 14, Appl
30	1225	97.2	288	6	US-11-018-102-1	Sequence 1, Appl
31	1225	97.2	288	6	US-11-129-083-14	Sequence 14, Appl
32	1225	97.2	288	6	US-11-128-495-14	Sequence 14, Appl
33	1225	97.2	288	6	US-11-128-496-14	Sequence 14, Appl
34	1225	97.2	288	6	US-11-129-080-14	Sequence 14, Appl
35	1225	97.2	288	6	US-11-128-709-14	Sequence 14, Appl
36	1225	97.2	329	4	US-10-370-749-48	Sequence 48, Appl
37	1225	97.2	329	5	US-10-798-380-37	Sequence 37, Appl
38	1225	97.2	330	3	US-09-995-898A-15	Sequence 15, Appl
39	1225	97.2	330	3	US-09-892-949-38	Sequence 38, Appl
40	1225	97.2	330	4	US-10-047-542-20	Sequence 20, Appl
41	1225	97.2	330	4	US-10-269-805-68	Sequence 68, Appl
42	1225	97.2	330	4	US-10-310-719-8	Sequence 8, Appl
43	1225	97.2	330	4	US-10-112-582-1	Sequence 1, Appl
44	1225	97.2	330	4	US-10-320-231A-81	Sequence 81, Appl
45	1225	97.2	330	4	US-10-383-902A-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-847-208-3
; Sequence 3, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-3

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Db	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF	60	
QY	61	NYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT	120	
Db	61	NYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT	120	
QY	121	ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180	
Db	121	ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP	180	
QY	181	PVLDSVGSFFLYSKLTVDKSRWQQGVNFVSCVMHEALHNHYQQRSLSPGK	232	
Db	181	PVLDSVGSFFLYSKLTVDKSRWQQGVNFVSCVMHEALHNHYQQRSLSPGK	232	

RESULT 2

US-10-000-439-3
; Sequence 3, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TREATMENT OF IMMUNE DISEASES

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; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000.439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-3

Query Match      100.0%; Score 1260; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 232

RESULT 3
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match      100.0%; Score 1260; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 219 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 232
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Db 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 330

RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000.439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match      100.0%; Score 1260; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.7e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
Qy 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSNKALPAPIEKT 218
Qy 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 180
Db 219 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 232
Db 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYQORSLSLSPGK 330

RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion between hinge-CH2-CH3 (IgG1) to CH2-CH3-CH4
; OTHER INFORMATION: (IGB)
US-09-847-208-7

Query Match      100.0%; Score 1260; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 6
US-10-000-439-7
; Sequence 7, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000,439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3
; OTHER INFORMATION: (IgG1) sequence and a CH2-CH3-CH4 (IgG) sequence
US-10-000-439-7

Query Match 100.0%; Score 1260; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 3.2e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 7
US-10-966-673-29
; Sequence 29, Application US/10966673
; Publication No. US20050226864A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R
; APPLICANT: Tsurushita, Naoya
; TITLE OF INVENTION: Alteration of Fc-Fusion Protein Serum Half-Lives By Mutagenesis
; FILE REFERENCE: 05882.0039.NPUS07
; CURRENT APPLICATION NUMBER: US/10/966,673

; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/562,627
; FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US 60/511,687
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 330
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-966-673-29

Query Match 97.5%; Score 1228; DB 5; Length 330;
Best Local Similarity 97.4%; Pred. No. 6.1e-90;
Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
Db 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 278
QY 181 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 279 PVLDSVGSFLLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 8
US-09-996-357-10
; Sequence 10, Application US/09996357
; Patent No. US20020133001A1
; GENERAL INFORMATION:
; APPLICANT: Geffer, Malcolm L
; APPLICANT: Joyal, John L
; APPLICANT: Gosselin, Michael
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
; FILE REFERENCE: PPI-105
; CURRENT APPLICATION NUMBER: US/09/996,357
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/253,302
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/250,198
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/257,186
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-357-10

Query Match 97.2%; Score 1225; DB 3; Length 232;
Best Local Similarity 97.0%; Pred. No. 7.1e-90;
Matches 325; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120


```
; APPLICANT: Wilkinson, Beverly
; TITLE OF INVENTION: SPEX COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: TSRI 810.1
; CURRENT APPLICATION NUMBER: US/10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 113
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-622-97

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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Db 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
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QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
   |||||
Db 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
   |||||

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
   |||||
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
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RESULT 13
US-10-800-497-26
; Sequence 26, Application US/10800497
; Publication No. US20040259209A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-
; TITLE OF INVENTION: stimulating factor with
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,497
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-497-26

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||
Db 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||

QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
   |||||
Db 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
   |||||

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
   |||||
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
   |||||

RESULT 14
US-10-800-449-26
; Sequence 26, Application US/10800449
; Publication No. US20040265973A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill
; APPLICANT: Sun, Cecily R
; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor
; TITLE OF INVENTION: increased biological activities
; FILE REFERENCE: 03SUN2001
; CURRENT APPLICATION NUMBER: US/10/800,449
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/09/968,362
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains
US-10-800-449-26

Query Match          97.2%; Score 1225; DB 5; Length 232;
Best Local Similarity 97.0%; Pred. No. 7,1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||
Db 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
   |||||

QY 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
   |||||
Db 61 NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
   |||||

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
   |||||
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQOQSLSLSPGK 232
   |||||

RESULT 15
US-10-964-215-97
; Sequence 97, Application US/10964215
; Publication No. US20050152893A1
; GENERAL INFORMATION:
; APPLICANT: Kaye, Jonathan
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE INHIBITION
; TITLE OF INVENTION: OF TRANSPLANT REJECTION
; FILE REFERENCE: TSRI 810.2
; CURRENT APPLICATION NUMBER: US/10/964,215
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/831,622
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/467,206
; PRIOR FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:58:19 ; Search time 12.0207 Seconds
(without alignments)
287.324 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNHYQQRSLSPGK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US05_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1225	97.2	232	6	US-10-948-053-1
2	1225	97.2	232	7	US-11-227-340-7
3	1225	97.2	251	7	US-11-242-294-6
4	1225	97.2	330	6	US-10-886-383-6
5	1225	97.2	330	6	US-10-493-909-20
6	1225	97.2	330	6	US-10-982-440-68
7	1225	97.2	330	7	US-11-022-289-11
8	1225	97.2	330	7	US-11-075-351-1
9	1225	97.2	330	7	US-11-165-141-15
10	1225	97.2	330	7	US-11-102-621-3
11	1225	97.2	330	7	US-11-102-621-7
12	1225	97.2	330	7	US-11-005-726-164
13	1225	97.2	330	7	US-11-124-620-1
14	1225	97.2	330	7	US-11-233-683-1
15	1225	97.2	335	7	US-11-024-251-35
16	1225	97.2	444	7	US-11-172-320-6
17	1225	97.2	444	7	US-11-173-969-6
18	1225	97.2	450	7	US-11-005-726-161
19	1225	97.2	450	7	US-11-049-536-701
20	1225	97.2	451	7	US-11-158-505-33
21	1225	97.2	451	7	US-11-124-620-7
22	1225	97.2	452	7	US-11-016-503-6
23	1225	97.2	459	6	US-10-949-720-390
24	1225	97.2	462	7	US-11-016-503-8
25	1225	97.2	470	7	US-11-072-512-3730

26	1225	97.2	476	7	US-11-139-499-4	Sequence 4, Appli
27	1225	97.2	476	7	US-11-139-499-12	Sequence 12, Appl
28	1225	97.2	478	7	US-11-139-499-8	Sequence 8, Appli
29	1225	97.2	551	7	US-11-022-289-7	Sequence 7, Appli
30	1225	97.2	551	7	US-11-022-289-8	Sequence 8, Appli
31	1225	97.2	557	7	US-11-016-503-4	Sequence 4, Appli
32	1225	97.2	557	7	US-11-022-289-4	Sequence 4, Appli
33	1225	97.2	557	7	US-11-022-289-5	Sequence 5, Appli
34	1225	97.2	557	7	US-11-022-289-6	Sequence 6, Appli
35	1225	97.2	567	7	US-11-016-503-2	Sequence 2, Appli
36	1225	97.2	567	7	US-11-016-503-10	Sequence 10, Appl
37	1225	97.2	641	7	US-11-227-340-8	Sequence 8, Appli
38	1225	97.2	679	7	US-11-227-340-11	Sequence 11, Appl
39	1225	97.2	701	7	US-11-227-340-6	Sequence 6, Appli
40	1225	97.2	771	6	US-10-949-720-389	Sequence 389, App
41	1223	97.1	592	6	US-10-016-686-4	Sequence 4, Appli
42	1222	97.0	330	7	US-11-102-621-71	Sequence 71, Appl
43	1222	97.0	446	7	US-11-102-621-121	Sequence 121, App
44	1222	97.0	447	7	US-11-102-621-132	Sequence 132, App
45	1220	96.8	330	7	US-11-102-621-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-10-948-053-1
; Sequence 1, Application US/10948053
; Publication No. US20060019887A1
; GENERAL INFORMATION:
; APPLICANT: Dunstan, Colin R.
; TITLE OF INVENTION: Compositions and Methods for the Prevention or Treatment of Canc
; TITLE OF INVENTION: Bone Loss Associated with Cancer
; FILE REFERENCE: A-605
; CURRENT APPLICATION NUMBER: US/10/948,053
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/389,545
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-948-053-1

Query Match	97.2%	Score 1225;	DB 6;	Length 232;
Best Local Similarity	97.0%;	Pred. No. 1.7e-101;		
Matches 225;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
Db	1	EPKSCDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
Qy	61	NWYDGVVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT	120	
Db	61	NWYDGVVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVSNKALPAPIEKT	120	
Qy	121	ISKAKVQREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180	
Db	121	ISKAKVQREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP	180	
Qy	181	PVLDSGVGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK	232	
Db	181	PVLDSGVGFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK	232	

RESULT 2
US-11-227-340-7
; Sequence 7, Application US/11227340
; Publication No. US20060024730A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E

```
; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: TF Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/11/227,340
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/10/617,619
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
US-11-227-340-7

Query Match          97.2%; Score 1225; DB 7; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.7e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60

Qy 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232

RESULT 3
US-11-242-294-6
; Sequence 6, Application US/11242294
; Publication No. US20060034852A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TAC1-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/11/242,294
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US/10/152,363
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-242-294-6

Query Match          97.2%; Score 1225; DB 7; Length 251;
Best Local Similarity 97.0%; Pred. No. 1.9e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 20 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 79

Qy 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
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Db 80 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 139
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 140 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 199
Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 200 PVLDSVGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 251

RESULT 4
US-10-886-383-6
; Sequence 6, Application US/10886383
; Publication No. US20060005571A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and use:
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,383
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-383-6

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 99 EPKSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 158

Qy 61 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
Db 159 NMVVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

Qy 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 279 PVLDSVGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 5
US-10-493-909-20
; Sequence 20, Application US/10493909
; Publication No. US20060015969A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING TOXICITY
; FILE REFERENCE: 41514-20004.01
; CURRENT APPLICATION NUMBER: US/10/493,909
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
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; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-493-909-20

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 158
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 330
```

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RESULT 6
US-10-982-440-68
; Sequence 68, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-68

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 158
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 330
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```
US-11-022-289-11
; Sequence 11, Application US/1102289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-68

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 158
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 330
```

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RESULT 7
US-11-022-289-11
; Sequence 11, Application US/1102289
; Publication No. US20050249723A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 68
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-68

Query Match          97.2%; Score 1225; DB 6; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 158
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 330
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; APPLICANT: Lazar, Gregory Alan
; TITLE OF INVENTION: FC POLYPEPTIDES WITH NOVEL FC LIGAND BINDING SITES
; FILE REFERENCE: 185831/US/2
; CURRENT APPLICATION NUMBER: US/11/022,289
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US 60/531,752
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 11
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-289-11

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 158
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
DB 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 330

RESULT 8
US-11-075-351-1
; Sequence 1, Application US/11075351
; Publication No. US20050260716A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Margaret D.
; APPLICANT: Fox, Brian A.
; TITLE OF INVENTION: DIMERIC FUSION PROTEINS AND MATERIALS
; FILE REFERENCE: 02-16
; CURRENT APPLICATION NUMBER: US/11/075,351
; CURRENT FILING DATE: 2005-03-08
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-351-1

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 60
DB 99 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDDEVKF 158
QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
DB 159 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYOQRSLSLSPGK 232
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RESULT 12
US-11-005-726-164
; Sequence 164, Application US/11005726
; Publication No. US20060018903A1
; GENERAL INFORMATION:
; APPLICANT: HELLEDOORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; TITLE OF INVENTION: TNF ALPHA-BINDING POLYPEPTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; FILE REFERENCE: MER-131
; CURRENT APPLICATION NUMBER: US/11/005,726
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: 10/495,146
; PRIOR FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: PCT/EP02/12566
; PRIOR FILING DATE: 2002-11-11
; PRIOR APPLICATION NUMBER: EP 01126858.8
; PRIOR FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-TNF alpha chimeric antibody heavy chain
; OTHER INFORMATION: constant region
US-11-005-726-164

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
   |||||
Db 99 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
   |||||
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 218

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 232
   |||||
Db 279 PVLDSGSGFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 330

RESULT 13
US-11-124-620-1
; Sequence 1, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
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; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-1

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
   |||||
Db 99 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
   |||||
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 218

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
   |||||
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278

QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 232
   |||||
Db 279 PVLDSGSGFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 330

RESULT 14
US-11-233-683-1
; Sequence 1, Application US/11233683
; Publication No. US20060025573A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/11/233,683
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-11-233-683-1

Query Match          97.2%; Score 1225; DB 7; Length 330;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60
   |||||
Db 99 EPKSCDKTHTCPPCPAPELLGSPVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 158

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 120
   |||||
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKVKSNKALPAPIEKT 218
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Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 278
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232
Db 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 330

RESULT 15
US-11-024-251-35
; Sequence 35, Application US/11024251
; Publication No. US20050266425A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Paris, Mark
; TITLE OF INVENTION: Methods for Producing and Identifying Multispecific Antibodies
; FILE REFERENCE: 1843.0230001
; CURRENT APPLICATION NUMBER: US/11/024,251
; CURRENT FILING DATE: 2004-12-29
; PRIOR APPLICATION NUMBER: 60/533,241
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: IgG Secreted Constant Domain
US-11-024-251-35

Query Match 97.2%; Score 1225; DB 7; Length 335;
Best Local Similarity 97.0%; Pred. No. 2.6e-101;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPPCPAPELIGGPSVFLPPPKPDTLMSRTPEVTCVVDVSHEDPEVKF 60
Db 104 EPKSCDKTHTCPPCPAPELIGGPSVFLPPPKPDTLMSRTPEVTCVVDVSHEDPEVKF 163
Qy 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 164 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 223
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
Db 224 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 283
Qy 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 232
Db 284 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQQRSLSLSPGK 335

Search completed: February 22, 2006, 22:03:44
Job time : 12.0207 secs
```

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OM protein - protein search, using sw model

Run on: February 22, 2006, 21:24:11 ; Search time 152.263 Seconds
(without alignments)
669.475 Million cell updates/sec

Title: US-10-000-439-3

Perfect score: 1260

Sequence: 1 EPKSCDKTHTCPPCPAPELL.....MHEALHNYQRRSLSPCK 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1260	100.0	232	6	AAO19665 Human Igg
2	1260	100.0	330	6	AAO19664 Human Igg
3	1260	100.0	569	6	AAO19668 GR2 fusio
4	1232	97.8	232	9	AD287506 Human Igg
5	1228	97.5	330	9	AD287506 Human Igg
6	1225	97.2	232	2	AAW26232 Human Igg
7	1225	97.2	232	3	AAW26232 Human Igg
8	1225	97.2	232	4	AAW26232 Human Igg
9	1225	97.2	232	4	AAW26232 Human Igg
10	1225	97.2	232	5	AAE15347 Human imm
11	1225	97.2	232	5	AAE15347 Human imm
12	1225	97.2	232	7	AD26272 Human Igg
13	1225	97.2	232	7	AD26272 Human Igg
14	1225	97.2	232	8	ADJ57512 Human Igg
15	1225	97.2	232	8	ADJ57512 Human Igg
16	1225	97.2	232	8	ADJ57512 Human Igg
17	1225	97.2	232	8	ADJ57512 Human Igg
18	1225	97.2	232	9	ADV99720 Human Igg
19	1225	97.2	232	9	ADV99720 Human Igg
20	1225	97.2	232	9	ADV99720 Human Igg
21	1225	97.2	232	9	ADV99720 Human Igg
22	1225	97.2	232	9	ADV99720 Human Igg
23	1225	97.2	232	9	ADV99720 Human Igg
24	1225	97.2	232	9	ADV99720 Human Igg

25	1225	97.2	235	6	ABJ38647	Abj38647 pCXFc pro
26	1225	97.2	235	6	ADA89055	Ada89055 Plasmid p
27	1225	97.2	235	7	ADD25647	Add25647 Binding d
28	1225	97.2	235	7	ADG74307	Adg74307 Fibroblas
29	1225	97.2	235	9	ADY21627	Ady21627 Human Igg
30	1225	97.2	247	5	AAE26274	Aae26274 Human bet
31	1225	97.2	251	5	ABB81490	Abb81490 Human imm
32	1225	97.2	251	6	AAE35214	Aae35214 Human wil
33	1225	97.2	259	2	AAE24154	Aay24154 Protein f
34	1225	97.2	267	5	AAE26273	Aae26273 Human tpa
35	1225	97.2	269	8	ADJ52120	Adj52120 CH1 delet
36	1225	97.2	285	9	AEA89551	Aea89551 Human imm
37	1225	97.2	287	4	AAW47590	Aaw47590 Fusion pr
38	1225	97.2	288	9	AEA89541	Aea89541 Human imm
39	1225	97.2	329	2	AAE1806	Aar1806 Human imm
40	1225	97.2	329	8	ADP56389	Adp56389 Human PRO
41	1225	97.2	329	8	ADS82579	Ads82579 Human Igg
42	1225	97.2	330	4	AAW4071	Aaw4071 Zcytor 10
43	1225	97.2	330	5	AAW47856	Aam47856 Human Ig-
44	1225	97.2	330	5	AAE21960	Aae21960 Human dea
45	1225	97.2	330	5	ABB81641	Abb81641 Human Igg

ALIGNMENTS

RESULT 1

AAO19665
ID AAO19665 standard; protein; 232 AA.

XX AAO19665;

XX 28-MAR-2003 (first entry)

XX Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.

XX Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
XX Fcepsilon receptor; autoimmune disease; constant region; heavy chain;
XX antiasthmatic; antiallergic; antiinflammatory; dermatological;
XX antiarthritic; antirheumatic; antidiabetic; neuroprotective;
XX hinge-CH2-CH3 region.

XX Homo sapiens.

XX WO200288317-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013527.

XX 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

XX (REGC) UNIV CALIFORNIA.

XX Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

XX New fusion molecules comprising polypeptide sequences that bind to IgG
XX Inhibitory receptor and native IGE receptor, useful for treating IGE-
XX mediated hypersensitivity reactions, e.g. asthma or allergies, or
XX autoimmune diseases.

XX Claim 19; Fig 3; 116pp; English.

XX The present invention relates to a fusion molecule comprising a first
XX polypeptide sequence capable of specific binding to a native Igg
XX polypeptide sequence consisting of an immune receptor tyrosine-based
XX inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
XX functionally connected to a second polypeptide sequence capable of
XX specific binding directly or indirectly to a native IGE receptor
XX (FcepsilonR). Also provided are nucleotide sequences encoding such a

CC fusion protein. The fusion molecules and compositions are useful for
 CC treating an IGE-mediated biological response, preferably an IGE-mediated
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
 CC or symptoms resulting from, a type I hypersensitivity reaction in a
 CC subject receiving immunotherapy. The present sequence is the human IgG1
 CC heavy chain constant region hinge-CH2-CH3 portion
 XX

SQ Sequence 232 AA;
 Query Match 100.0%; Score 1260; DB 6; Length 232;
 Best Local Similarity 100.0%; Pred. No. 3.3e-91;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 180
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQQRSLSPGK 232
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQQRSLSPGK 232

RESULT 2
 AAO19664
 ID AAO19664 standard; protein; 330 AA.
 XX
 AC AAO19664;

DT 28-MAR-2003 (first entry)
 DE Human IgG1 heavy chain constant region.
 XX
 KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;
 KW Fcεpsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological;
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.
 XX

OS Homo sapiens.
 XX
 FN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 XX
 PR 01-MAY-2001; 2001US-00847208.
 PR 24-OCT-2001; 2001US-00000439.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX

FI Saxon A, Zhang K, Zhu D;
 XX
 DR WPI; 2003-103456/09.
 XX
 PT New fusion molecules comprising polypeptide sequences that bind to IgG
 PT inhibitory receptor and native IGE receptor, useful for treating IGE-
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
 PT autoimmune diseases.
 XX
 PS Claim 64; Fig 2; 116pp; English.
 XX
 CC The present invention relates to a fusion molecule comprising a first

CC polypeptide sequence capable of specific binding to a native IgG
 CC inhibitory receptor consisting of an immune receptor tyrosine-based
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
 CC functionally connected to a second polypeptide sequence capable of
 CC specific binding directly or indirectly to a native IGE receptor
 CC (FcεpsilonR). Also provided are nucleotide sequences encoding such a
 CC fusion protein. The fusion molecules and compositions are useful for
 CC treating an IGE-mediated biological response, preferably an IGE-mediated
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
 CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
 CC or symptoms resulting from, a type I hypersensitivity reaction in a
 CC subject receiving immunotherapy. The present sequence is the human IgG1
 CC heavy chain constant region
 XX

SQ Sequence 330 AA;
 Query Match 100.0%; Score 1260; DB 6; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5.1e-91;
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
 DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 218
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 180
 DB 219 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTT 278
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQQRSLSPGK 232
 DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQQRSLSPGK 330

RESULT 3
 AAO19668
 ID AAO19668 standard; protein; 569 AA.
 XX
 AC AAO19668;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE GE2 fusion protein for use in treating immune diseases.
 XX

Human; IgG; immunoglobulin E; immunotherapy; immune disease;
 KW Fcεpsilon receptor; autoimmune disease; constant region; heavy chain;
 KW antiasthmatic; antiallergic; antiinflammatory; dermatological; GE2;
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;
 KW fusion protein.
 XX

OS Synthetic.
 OS Unidentified.
 XX
 FN WO200288317-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 01-MAY-2002; 2002WO-US013527.
 XX
 PR 01-MAY-2001; 2001US-00847208.
 PR 24-OCT-2001; 2001US-00000439.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 FI Saxon A, Zhang K, Zhu D;
 XX
 DR WPI; 2003-103456/09.
 XX

PT New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IGE receptor, useful for treating Ige-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
XX autoimmune diseases.
PS Claim 35; Fig 7; 116pp; English.
XX
CC The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IgG
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IGE receptor
CC (FcεpsilonR). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC treating an Ige-mediated biological response, preferably an Ige-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is a gammahinge-
CC CHgamma2-CHgamma3-(Gly4Ser)3-Chepsilon2-Chepsilon3 fusion
CC protein (designated G52) of the invention
XX
SQ Sequence 569 AA;
Query Match 100.0%; Score 1260; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 9.7e-91;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTPRREQYNSTYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTPRREQYNSTYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
RESULT 4
ADZ87506
ID ADZ87506 standard; protein; 232 AA.
XX
AC ADZ87506;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human IgG1 protein region SeqID33.
XX
KW protein engineering; immunoglobulin; cytostatic; cancer.
XX
OS Homo sapiens.
XX
PN WO2005042573-A1.
XX
PD 12-MAY-2005.
XX
PF 21-OCT-2004; 2004WO-US034680.
XX
PR 24-OCT-2003; 2003US-0514198P.
XX
PR 12-NOV-2003; 2003US-0519822P.
XX
XX (DAND) DANA FARBER CANCER INST INC.
PA (ILEX-) ILEX PROD INC.

XX Kharbanda S, Kufe DW;
XX WPI: 2005-346855/35.
DR N-PSDB; ADZ87507.
XX
PT MUC1 ligand trap comprising a MUC1 extracellular polypeptide and an
PT immunoglobulin FC polypeptide or an albumin polypeptide, useful for
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 33; 82pp; English.
XX
CC This invention relates to a novel MUC1 chimeric protein which comprises a
CC first polypeptide sequence and a second polypeptide sequence, where the
CC first polypeptide sequence is a MUC1 extracellular (MUC1-EC) polypeptide,
CC and the second polypeptide sequence is a human immunoglobulin FC
CC polypeptide or a human albumin polypeptide. The invention may be useful
CC for the development of compounds with a cytostatic activity acting as
CC MUC1 antagonists or CD227 antagonists. The MUC1 chimeric protein is
CC useful in preparing a composition for treating cancer. The present
CC sequence is that of a protein which was used during the development of
CC the novel MUC1 chimeric protein of the invention.
XX
SQ Sequence 232 AA;
Query Match 97.8%; Score 1232; DB 9; Length 232;
Best Local Similarity 97.4%; Pred. No. 5.4e-89;
Matches 226; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 1 EPKSCDKHTCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NNYVDGVEVHNKTPRREQYNSTYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
DB 61 NNYVDGVEVHNKTPRREQYNSTYRVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
DB 181 PVLDSVGSFPLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
RESULT 5
ADZ69628
ID ADZ69628 standard; protein; 330 AA.
XX
AC ADZ69628;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human IgG1 heavy chain constant region, mutant L314M.
XX
KW Heavy chain constant region; antibody engineering; protein engineering;
KW immunoglobulin; mutein; fusion protein; cancer; cytostatic; neoplasm;
KW autoimmune disease; immunosuppressive; immune disorder.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 197 /note= "Wild-type Leu substituted by Met"
XX
XX WO2005037867-A1.
XX
XX 28-APR-2005.
XX
XX 15-OCT-2004; 2004WO-US034440.
XX
XX

PR 15-OCT-2003; 2003US-0511687P.
 PR 14-APR-2004; 2004US-0562627P.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 XX Hinton PR, Tsurushita N;
 PI WPI; 2005-315683/32.
 DR
 XX
 XX New modified Fc-fusion protein where at least one amino acid residue from
 PT the heavy chain constant region, useful for studying protein function in
 PT vitro and in vivo and as potential therapeutic and diagnostic agents.
 XX
 XX Claim 21; SEQ ID NO 29; 170pp; English.
 XX
 CC The invention relates to a modified Fc-fusion protein where at least one
 CC amino acid residue from the heavy chain constant region selected from
 CC residues 250, 314, and 428 (Kabat numbering) is different from that
 CC present in the unmodified Fc-fusion protein. Also included are an Fc-
 CC fusion protein comprising an Fc region substantially identical to that of
 CC a naturally occurring class Igg antibody, a modified Fc-fusion protein
 CC with an in vivo mean elimination half-life at least about 1.3-fold longer
 CC than that of the corresponding unmodified Fc-fusion protein, a modified
 CC Igg class antibody fragment (comprising a heavy chain constant region or
 CC Fc-region where at least one amino acid residue selected from the group
 CC consisting of residues 250, 314, and 428 is different from that present
 CC in the unmodified Igg class antibody), an isolated polynucleotide
 CC molecule encoding a polypeptide comprising a sequence at least 90%
 CC identical to a sequence selected from AD269600-AD269656, an isolated
 CC polypeptide comprising an amino acid sequence at least 90% identical to a
 CC sequence selected from AD269600-AD269656, a method for altering FcRn
 CC binding affinity/serum half-life of an Fc-fusion protein (comprising
 CC selecting at least one amino acid residue as cited above, and
 CC substituting the selected residue(s) with an amino acid different from
 CC that present in the Fc-fusion protein) and a method of producing a
 CC modified Fc-fusion protein with an altered binding affinity for
 CC FcRn/alters serum half-life as compared with the unmodified Fc-fusion
 CC protein (comprising preparing an expression vector comprising a suitable
 CC promoter operably linked to DNA encoding at least a constant region of an
 CC Igg heavy chain, transforming host cells with the vector and culturing
 CC the transformed host cells to produce the modified Igg Fc fusion
 CC protein). The modified antibody has a higher affinity for FcRn at pH 6.0
 CC than at pH 8.0. The fusion proteins are useful for studying protein
 CC function in vitro and in vivo and as potential therapeutic and diagnostic
 CC agents. The present sequence represents a human Igg1 heavy chain constant
 CC region with an amino acid substitution at residue 250, 314 or 428 (Kabat
 CC numbering, the actual residue that is mutated is covered in the feature
 CC table).

XX SQ Sequence 330 AA;
 Query Match 97.5%; Score 1228; DB 9; Length 330;
 Best Local Similarity 97.4%; Pred. No. 1.7e-88;
 Matches 226; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWMMNGKEYCKCKVSNKALPAPIEKT 120
 DB 159 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWMMNGKEYCKCKVSNKALPAPIEKT 218
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 DB 219 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSLSPGK 232
 DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSLSPGK 330

RESULT 6

AAW26232
 ID AAW26232 standard; protein; 232 AA.
 XX
 AC AAW26232;
 XX
 DT 16-MAR-1998 (first entry)
 XX
 DE Human IgG1 hinge/Fc region.
 XX
 KW Fusion protein; hydrophilic spacer; recombinant; expression system;
 KW carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.
 OS Homo sapiens.
 XX
 XX WO9728272-A1.
 FN
 XX
 PD 07-AUG-1997.
 XX
 XX 31-JAN-1997; 97WO-US001470.
 PF
 XX
 XX 31-JAN-1996; 96US-00595043.
 PR
 XX (TECH-) TECHNOLOGENE INC.
 PA
 XX Sgarlato GD;
 PI
 XX WPI; 1997-402624/37.
 DR N-PSDB; AAT80158.
 XX
 XX Recombinant protein expression system for fusion protein production -
 PT useful for high quantity production of authentic recombinant proteins.
 PT
 PS Example 3; Page 133-134; 194pp; English.
 XX
 CC A novel recombinant vector has been developed which comprises a
 CC nucleotide sequence encoding a fusion protein. The fusion protein
 CC comprises three domains joined together in order, from N-terminus to C-
 CC terminus, of a first domain comprising a protein of interest, a second
 CC domain comprising a hydrophilic spacer and an affinity domain, each
 CC domain comprising amino acid residues. The present sequence represents
 CC the hinge/Fc region of human IgG1, used in example 3 of the present
 CC invention. The recombinant vector is used for the production of authentic
 CC recombinant proteins of interest. The method of the invention is useful
 CC for the expression of fusion proteins capable of isolation by affinity
 CC chromatography in pro- or eukaryotic cells. This method allows for the
 CC efficient cleavage and generation of authentic proteins of interest that
 CC do not contain extraneous (i.e. non-naturally occurring) amino acids
 XX
 XX SQ Sequence 232 AA;
 Query Match 97.2%; Score 1225; DB 2; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWMMNGKEYCKCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWMMNGKEYCKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSLSPGK 232
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSLSPGK 232

RESULT 7
 AAB28690

AA28690 standard; protein; 232 AA.
AA28690;
14-FEB-2001 (first entry)
Human IgGgamma hinge, CH2 and CH3 regions.
Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
transplant rejection; cardiovascular disease; arteriosclerosis;
IgGgamma.
Homo sapiens.
WO200063253-A1.
26-OCT-2000.
24-MAR-2000; 2000WO-US008004.
16-APR-1999; 99US-00293245.
(AMGE-) AMGEN INC.
Hsu H, Meng S;
WPI; 2000-665240/64.
Fusion protein of AGP-1 protein and an Fc region, used to treat
proliferative disorders, immune disorders, and virally-induced disorders.
Claim 2; Fig 1; 93pp; English.
The present sequence was used in the production of AGP-1 fusion proteins.
AGP-1 is a type II transmembrane protein. The fusion proteins comprise an
Fc immunoglobulin region fused to the N-terminal portion of the AGP-1
protein. The fusion proteins can be used to induce apoptosis in a tissue,
and to treat proliferative disorders, immune disorders, or virally-
induced disorders. The proliferative disorders include cancers, such as
breast, prostate, lung or colon cancer. The viral infections include
hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune
disorders may be autoimmune disorders or transplant rejection.
Cardiovascular diseases such as arteriosclerosis may also be treated. The
AGP-1 containing fusion proteins have increased biological activity
compared to the soluble AGP-1 proteins used in prior art therapies

Query Match 97.2%; Score 1225; DB 3; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.9e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPP 180
Db 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 8

AA280897
ID AAB80897 standard; protein; 232 AA.
XX AAB80897;
XX 31-MAY-2001 (first entry)
XX Human IgGgamma hinge, CH2 and CH3 regions.
XX Human; IgGgamma; anticancer; Antimetastatic; Osteogenic;
XX lytic bone disease; multiple myeloma; immunoglobulin;
XX osteosclerotic bone metastasis; OPG; osteoprotegerin;
XX osteoclast formation inhibition; bone resorption inhibition.
XX OS Homo sapiens.
XX PN WO200117543-A2.
XX PD 15-MAR-2001.
XX PF 18-AUG-2000; 2000WO-US022806.
XX PR 03-SEP-1999; 99US-00389545.
XX PA (AMGE-) AMGEN INC.
XX PI Dunstan CR;
XX DR WPI; 2001-265936/27.
XX PT Preventing or treating lytic bone diseases, particularly associated with
XX cancer or metastasis, by administering an osteoprotegerin polypeptide.
XX PS Disclosure; Fig 1; 87pp; English.
XX CC The present invention relates to a method for the prevention or treatment
XX of lytic bone disease or multiple myeloma. Also the method can be used
XX for preventing metastasis of cancer to bone or osteosclerotic bone
XX metastasis. The method comprises administering an OPG (osteoprotegerin)
XX polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-
XX AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)
XX by blocking differentiation from monocytes/macrophage precursors. The
XX present sequence is the hinge, CH2 and CH3 regions of human IgGgamma.
XX This sequence can be used to generate fusion proteins of OPG and
XX immunoglobulin, for use in the present invention. The generated fusion
XX proteins can exhibit increased circulating half-lives and slower
XX clearance times, thereby providing a more sustained activity

Query Match 97.2%; Score 1225; DB 4; Length 232;
Best Local Similarity 97.0%; Pred. No. 1.9e-88;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHCTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQWNMNGKEYCKVSNKALPAPIEKT 120
Db 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDNLNGKEYCKVSNKALPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPP 180
Db 121 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232
Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 9
AA272915

ID	AA72915	standard; protein; 232 AA.
XX	AA72915;	
AC		
XX		
DT	13-JUN-2001	(first entry)
XX		
DE	Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.	
XX		
XX	Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;	
KW	therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;	
KW	hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;	
KW	osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;	
KW	periodontal.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200118203-A1.	
XX		
PD	15-MAR-2001.	
XX		
PF	18-AUG-2000; 2000WO-US022797.	
XX		
PR	03-SEP-1999; 99US-00389782.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Dunstan CR, Wooden SK, Mann MB;	
XX		
DR	WPI; 2001-244572/25.	
XX		
PT	Osteoprotegerin-Fc protein fusions useful for treating bone loss caused	
PT	by e.g. osteoporosis, Paget's disease and osteomyelitis.	
XX		
PS	Claim 3; Fig 1; 119pp; English.	
XX		
CC	The patent discloses fusion protein comprising human osteoprotegerin	
CC	(OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively	
CC	regulates formation of osteoclasts in vitro and in vivo. It blocks the	
CC	differentiation of osteoclasts from monocyte or macrophage precursors and	
CC	the reabsorption of bone. The OPG-Fc fusion protein is administered for	
CC	the treatment of bone loss resulting from osteoporosis, Paget's disease,	
CC	osteomyelitis, hypercalcaemia, osteopenia associated with surgery or	
CC	steroid administration, osteonecrosis, bone loss due to rheumatoid	
CC	arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic	
CC	loosening. The present sequence is partial human immunoglobulin G (Ig G)	
CC	1 protein comprising the hinge and heavy chain constant regions CH2 and	
CC	CH3	
XX		
SQ	Sequence 232 AA;	
Query Match 97.2%; Score 1225; DB 4; Length 232;		
Best Local Similarity 97.0%; Pred. No. 1.9e-88;		
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
Qy	1	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db	1	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Qy	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLQHNWMNGKEYCKVSNKALPAPIEKT 120
Db	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLQHNWMNGKEYCKVSNKALPAPIEKT 120
Qy	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db	121	ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
Db	181	PVLDSGGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
RESULT 10		
AAE15347		
ID	AAE15347	standard; protein; 232 AA.
XX	AAE15347;	
AC		
XX		
DT	09-APR-2002	(first entry)
XX		
DE	Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.	
XX		
KW	Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG;	
KW	cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200181405-A2.	
XX		
PD	01-NOV-2001.	
XX		
PF	19-APR-2001; 2001WO-US012836.	
XX		
PR	21-APR-2000; 2000US-00559001.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Egrie JC, Elliott SG, Browne JK, Sitney KC;	
XX		
DR	WPI; 2002-034433/04.	
XX		
PT	Increasing and maintaining hematocrit in mammal suffering from anemia,	
PT	comprising administering hyperglycosylated analog of erythropoietin less	
PT	frequently and at lower molar amount of recombinant human erythropoietin.	
XX		
PS	Example 1; Fig 10; 95pp; English.	
XX		
CC	The invention relates to a method for increasing and maintaining	
CC	haematocrit in a mammal. The method comprises administering a	
CC	hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical	
CC	composition, less frequently than an equivalent molar amount of and at a	
CC	lower molar amount than recombinant human Epo (rHuEpo) to obtain a	
CC	comparable target haematocrit. Epo is a glycoprotein hormone necessary	
CC	for the maturation of erythroid progenitor cells into erythrocytes. Human	
CC	Epo analogue is useful for raising and maintaining haematocrit to a	
CC	comparable target haematocrit in a mammal suffering from anaemia	
CC	associated with a decline or loss of kidney function, myelosuppressive	
CC	therapy comprising chemotherapeutic or anti-viral drugs or associated	
CC	with excessive blood loss during surgical procedures, and in cancer	
CC	condition. The present sequence is human immunoglobulin G (IgG) gamma 1	
CC	constant heavy chain (CH2, CH3) hinge region used to construct Epo	
CC	hyperglycosylated analogue fusion protein	
XX		
SQ	Sequence 232 AA;	
Query Match 97.2%; Score 1225; DB 5; Length 232;		
Best Local Similarity 97.0%; Pred. No. 1.9e-88;		
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;		
Qy	1	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db	1	EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Qy	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLQHNWMNGKEYCKVSNKALPAPIEKT 120
Db	61	NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLQHNWMNGKEYCKVSNKALPAPIEKT 120
Qy	121	ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db	121	ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Qy	181	PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYQOQSLSLSPGK 232
Db	181	PVLDSGGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
RESULT 11		
AAE15347		

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMEALHNHYTQKSLSLSPGK 232

RESULT 13
 ADJ57512
 ID ADJ57512 standard; protein; 232 AA.
 XX
 AC ADJ57512;
 XX
 DT
 XX
 DE Human IgG1 Fc domain fragment.
 XX
 KW TF, tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;
 KW cerebroprotective; cytostatic; vasotropic; anti-rheumatic; anti-arthritis;
 KW anti-arteriosclerotic; anti-inflammatory; antibacterial; immunosuppressive;
 KW hypertensive; cardiac; coagulation Factor VII; human; immunoglobulin G1;
 KW IgG1.
 XX
 OS Homo sapiens.
 XX
 FN WO2004006962-A2.
 XX
 PD 22-JAN-2004.
 XX
 PF 09-JUL-2003; 2003WO-DK000481.
 XX
 PR 12-JUL-2002; 2002DK-00001099.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 FI Bjorn SE, Nicolaisen EM, Steenstrup TD;
 XX
 DR WPI; 2004-180224/17.
 XX
 PT New compound binding to tissue factor, useful for treating diseases such
 as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.
 XX
 PS Claim 16; SEQ ID NO 7; 61pp; English.
 XX

The invention relates to a compound (I) binding to tissue factor (TF).
 The compound (I) has the formula A-(LM)-C, where A is a FVIIa
 polypeptide, LM is an optional linker group, C comprises an
 immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-
 mediated activated factor VII (FVIIa) activity. (I) is useful as a
 medicament, and for the manufacture of a medicament for preventing or
 treating disease or disorder associated with pathophysiological TF
 activity. The disease or disorder associated with pathophysiological TF
 activity are deep venous thrombosis, arterial thrombosis, post surgical
 thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal
 coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,
 angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis,
 arteriosclerosis and restenosis following angioplasty, acute and chronic
 indications such as inflammation, septic shock, septicemia, hypotension,
 adult respiratory distress syndrome (ARDS), disseminated intravascular
 coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial
 infarction, or prophylactic treatment of mammals with atherosclerotic
 vessels at risk for thrombosis. The present sequence represents the Fc
 domain fragment of human immunoglobulin G1 (IgG1).

Sequence 232 AA;
 Query Match 97.2%; Score 1225; DB 8; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

DB 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
 QY 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120
 DB 61 NMYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMEALHNHYTQKSLSLSPGK 232

RESULT 14
 ADR48992
 ID ADR48992 standard; peptide; 232 AA.
 XX
 AC ADR48992;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human IgG1 hinge and CH2 region.
 XX
 KW antianaemic; nephrotropic; human; HuEPO-L-vFc; erythropoietin; EPO;
 KW anaemia; renal disease; cancer chemotherapy; rheumatoid arthritis;
 KW AZT treatment; HIV infection; myelodysplastic syndrome; renal failure.
 XX
 OS Homo sapiens.
 XX
 FN US2004175824-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 21-JAN-2004; 2004US-00761593.
 XX
 PR 17-AUG-2001; 2001US-00932812.
 XX
 PA (SUNL/) SUN L K.
 PA (SUNB/) SUN B N C.
 PA (SUNC/) SUN C R Y.
 XX
 PI Sun LK, Sun BNC, Sun CRY;
 XX
 DR WPI; 2004-634851/61.
 XX
 PT New recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
 (HuEPO), a peptide linker, and a human Igg Fc variant, useful for
 treating chronic anemia due to renal diseases, cancer chemotherapy, or
 rheumatoid arthritis.
 XX
 PS Disclosure; SEQ ID NO 26; 31pp; English.
 XX
 CC A recombinant HuEPO-L-vFc fusion protein comprises human erythropoietin
 (HuEPO), a peptide linker, and a human Igg Fc variant, is new.
 CC INDEPENDENT CLAIMS are also included for the following: a chinese hamster
 ovary (CHO)-derived cell line producing the HuEPO-L-vFc fusion protein in
 its growth medium in excess of 10 microg per million cells in a 24 hour
 period; and a method for making a recombinant fusion protein comprising
 HuEPO, a flexible peptide linker, and a human Igg Fc variant. Preferred
 Protein: The peptide linker containing 20 or fewer amino acids is present
 between HuEPO and the human Igg Fc variant, and comprises two or more
 amino acids selected from glycine, serine, alanine, and threonine. The
 human Igg Fc variant comprises a hinge, CH2, and CH3 domains of human
 IgG2 with Pro331Ser mutation comprising 436 amino acids (SEQ ID NO. 18).
 CC It also comprises a hinge, CH2, and CH3 domains of human IgG4 with
 Ser228Pro and Leu235Ala mutations comprising 437 amino acids (SEQ ID NO.
 CC 20). It further comprises a hinge, CH2, and CH3 domains of human IgB1
 CC with Leu234Val, Leu235Ala, and Pro331Ser mutations comprising 435 amino
 CC acids (SEQ ID NO. 22). The HuEPO-L-vFc fusion protein exhibits in vitro
 CC biological activity similar to or higher than that of rHuEPO on a molar

CC basis. Preferred CHO-Derived Cell Line: The CHO-derived cell line
 CC producing the HuEPO-L-vfc fusion protein in its growth medium in excess
 CC of 30 μ mol/g per million cells in a 24 hour period. The human IgG Fc
 CC variant comprises a hinge, CH2, CH3 domains of human IgG selected from
 CC IgG1 as SEQ ID NO. 22, IgG2 as SEQ ID NO. 18, and IgG4 as SEQ ID NO. 20,
 CC the IgG Fc contains amino acid mutations to attenuate effector functions,
 CC a flexible peptide linker containing 20 or fewer amino acids is present
 CC between HuEPO and human IgG Fc variant, and the HuEPO-L-vfc fusion
 CC protein exhibits in vitro biological activity similar to or higher than
 CC that of rHuEPO on a molar basis. Preferred Method: Making a recombinant
 CC fusion protein comprising HuEPO, a flexible peptide linker, and a human
 CC IgG Fc variant comprises: generating a CHO-derived cell line; growing the
 CC cell line where the recombinant protein is expressed in its growth medium
 CC in excess of 10 μ mol/g per million cells in a 24 hour period; and
 CC purifying the expressed protein from (b), where the recombinant fusion
 CC protein exhibits in vitro biological activity similar to or higher than
 CC that of rHuEPO on a molar basis. Antianemic; Nephrotropic. No biological
 CC data given. None given. Administration can be through subcutaneous or
 CC intravenous route. No dosage given. The recombinant HuEPO-L-vfc fusion
 CC protein is useful for treating patients with chronic anemia due to renal
 CC diseases, cancer chemotherapy, rheumatoid arthritis, AZT treatment for
 CC HIV infection, or myelodysplastic syndrome. It is also useful in the
 CC treatment of renal failure. A fusion protein was assembled from several
 CC DNA segments. To obtain the gene encoding the leader peptide and mature
 CC protein of human erythropoietin (EPO), cDNA library of human fetal liver
 CC or kidney was used as the template in polymerase chain reaction (PCR).
 CC For the convenience of cloning, SEQ ID NO. 1 which incorporates a
 CC restriction enzyme cleavage site is used as the 5' oligonucleotide
 CC primer. The 3' primer (SEQ ID NO. 2) eliminates the EPO termination codon
 CC and incorporates a BamHI site. The resulting DNA fragments of
 CC approximately 600 bp were inserted into a holding vector such as pUC19 at
 CC the HindIII and BamHI sites to give the pEPO plasmid. The sequence of the
 CC human EPO gene was confirmed by DNA sequencing.

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232

RESULT 15

ADU51146
 ID ADU51146 standard; protein; 232 AA.

XX AC ADU51146;

XX DT 27-JAN-2005 (first entry)

XX DE Human spleen-expressed receptor-related solubility-promoting protein.

XX KW immunosuppressive; cytostatic; antiinflammatory; immune modulation;
 KW intercellular communication; autoimmune disease; cancer; neoplasm;
 KW transplant rejection; immune disorder; inflammation; gene therapy.

XX OS Homo sapiens.

PN WO2004096976-A2.
 XX 11-NOV-2004.
 XX 29-APR-2004; 2004WO-EP004562.
 XX 30-APR-2003; 2003US-0467206P.
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS PHARMA GMBH.
 XX (SCRI) SCRIPPS RES INST.
 XX Kaye J, Wilkinson B;
 XX WPI; 2004-804740/79.

XX New purified spleen expressed (SPFX) polypeptide useful for modulating
 XX lymphocyte activation and the immune response in disorders including
 XX autoimmunity, cancer, transplant rejection and inflammation.

XX Disclosure; SEQ ID NO 97; 98pp; English.

XX The invention relates to a novel purified polypeptide comprising any of
 CC SEQ ID NOS: 3, 7, 9, 11, 45 or 88, or an amino acid sequence that is 95%
 CC or more identical to the amino acid sequences and which includes an
 CC immunoglobulin like domain structure. The polypeptide of the invention
 CC demonstrates immunosuppressive, cytostatic and antiinflammatory
 CC activities and is a spleen-expressed (SPFX) polypeptide. The methods and
 CC compositions of the present invention may be useful for modulating
 CC lymphocyte activation and the immune response in a variety of conditions
 CC including autoimmunity, cancer, transplant rejection and inflammation.
 CC Such modulation may be achieved via the use of gene therapy. The current
 CC sequence is that of the human spleen-expressed (SPFX) receptor-related
 CC solubility-promoting protein of the invention.

XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 8; Length 232;
 Best Local Similarity 97.0%; Pred. No. 1.9e-88;
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 DB 1 EPKSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
 DB 181 PVLDSGDSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232

Search completed: February 22, 2006, 21:30:46
 Job time : 155.263 secs

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